- 1 -

SEQUENCE LISTING

<110> Melbourne Health
       Jane , Stephen (US Only)
       Wilanowski, Tomasz (US only)
       Ting, Stephen (US only)

<120> Diagnostic and Therapeutic Agents

<130> 12301370/EJH

<150> US 60/402055
<151> 2002-08-09

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<151> 2002-08-22

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<170> PatentIn version 3.1

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ccc cag cag tgt atc atc ctg agc cca ctg agc ggg tgg tgg ttt tcg   162
Pro Gln Gln Cys Ile Ile Leu Ser Pro Leu Ser Gly Trp Trp Phe Ser
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atc gga atc tca ata ctg acc agt tca gct ctg gtg ctc aag ccc caa   210
Ile Gly Ile Ser Ile Leu Thr Ser Ser Ala Leu Val Leu Lys Pro Gln
 25   30   35

atg ctc aaa ggc gaa ctc cag act cga cct tct cag aga cct tca agg   258
Met Leu Lys Gly Glu Leu Gln Thr Arg Pro Ser Gln Arg Pro Ser Arg
 40   45   50   55

aag gcg ttc agg agg aac aac ttt gaa tat acc cta gaa gct tca aaa   306
Lys Ala Phe Arg Arg Asn Asn Phe Glu Tyr Thr Leu Glu Ala Ser Lys
                     60   65   70

tca ctt cga cag aag cca gga gac agt acc atg acg tac ctg aac aaa   354
Ser Leu Arg Gln Lys Pro Gly Asp Ser Thr Met Thr Tyr Leu Asn Lys

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ggc cag ttc tat ccc atc acc ttg aag gag gtg agc agc agt gaa gga    402
Gly Gln Phe Tyr Pro Ile Thr Leu Lys Glu Val Ser Ser Ser Glu Gly
          90                      95                     100

atc cat cat ccc atc agc aaa gtt cga agt gtg atc atg gtg gtt ttt    450
Ile His His Pro Ile Ser Lys Val Arg Ser Val Ile Met Val Val Phe
         105                     110                     115

gct gaa gac aaa agc aga gaa gat cag tta agg cat tgg aag tac tgg    498
Ala Glu Asp Lys Ser Arg Glu Asp Gln Leu Arg His Trp Lys Tyr Trp
120                     125                     130                135

cac tcc cgg cag cac acc gct aaa caa aga tgc att gac ata gct gac    546
His Ser Arg Gln His Thr Ala Lys Gln Arg Cys Ile Asp Ile Ala Asp
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tat aaa gaa agc ttc aac act atc agt aac atc gag gag att gcg tat    594
Tyr Lys Glu Ser Phe Asn Thr Ile Ser Asn Ile Glu Glu Ile Ala Tyr
                     155                     160                     165

aac gcc att tcc ttc aca tgg gac atc aac gat gaa gca aag gtt ttc    642
Asn Ala Ile Ser Phe Thr Trp Asp Ile Asn Asp Glu Ala Lys Val Phe
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atc tct gtg aac tgc tta agc aca gat ttc tct tcc cag aag gga gtg    690
Ile Ser Val Asn Cys Leu Ser Thr Asp Phe Ser Ser Gln Lys Gly Val
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Lys Gly Leu Pro Leu Asn Ile Gln Val Asp Thr Tyr Ser Tyr Asn Asn
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cgc agc aac aag cct gtg cac cgg gcc tac tgc cag atc aag gtc ttc    786
Arg Ser Asn Lys Pro Val His Arg Ala Tyr Cys Gln Ile Lys Val Phe
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tgt gac aag gga gct gag cgg aaa atc agg gat gaa gaa cga aag caa    834
Cys Asp Lys Gly Ala Glu Arg Lys Ile Arg Asp Glu Glu Arg Lys Gln
                 235                     240                     245

agc aaa aga aaa gtt tct gat gtt aaa gtg cca ctg ctt ccc tct cac    882
Ser Lys Arg Lys Val Ser Asp Val Lys Val Pro Leu Leu Pro Ser His
         250                     255                     260

aag cga atg gat atc aca gtt ttc aaa ccc ttc att gat ctc gat act    930
Lys Arg Met Asp Ile Thr Val Phe Lys Pro Phe Ile Asp Leu Asp Thr
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cag cct gtc ctc ttc att cct gac gtg cac ttt gcc aac ttg cag cgg    978
Gln Pro Val Leu Phe Ile Pro Asp Val His Phe Ala Asn Leu Gln Arg
280                     285                     290                295

ggc act cat gtc ctt ccc att gcc tct gaa gaa ttg gag ggt gaa ggc   1026
Gly Thr His Val Leu Pro Ile Ala Ser Glu Glu Leu Glu Gly Glu Gly
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-3-

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Ser Val Leu Lys Arg Gly Pro Tyr Gly Thr Glu Asp Asp Phe Ala Val
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cct cct tct acc aag ctg gcc cgg ata gaa gaa cca aag aga gtg ctg      1122
Pro Pro Ser Thr Lys Leu Ala Arg Ile Glu Glu Pro Lys Arg Val Leu
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ctc tac gtt cga aag gag tca gaa gaa gtc ttt gat gcc ctg atg ctc      1170
Leu Tyr Val Arg Lys Glu Ser Glu Glu Val Phe Asp Ala Leu Met Leu
            345             350             355

aaa acc cca tct ttg aag ggc ttg atg gaa gct atc tca gac aaa tac      1218
Lys Thr Pro Ser Leu Lys Gly Leu Met Glu Ala Ile Ser Asp Lys Tyr
360             365             370             375

gat gtt ccc cat gac aag att ggg aaa ata ttc aag aag tgt aaa aag      1266
Asp Val Pro His Asp Lys Ile Gly Lys Ile Phe Lys Lys Cys Lys Lys
            380             385             390

ggg atc ctg gtg aac atg gac gac aac att gtg aag cat tac tcc aat      1314
Gly Ile Leu Val Asn Met Asp Asp Asn Ile Val Lys His Tyr Ser Asn
            395             400             405

gag gac acc ttccagctgc agattgaaga agccgggggg tcttacaagc              1363
Glu Asp Thr
            410

tcaccctgac ggagatctaa aggcctgcgg gccacagctc cccaggagtt cagtgcaggt     1423

gtttctagat cttacggttt ggcaactgca ggtaacccca gtcagccatg tcgccagcac     1483

aggtctatgt cgagggaatg ggttccttgc aggttggagg cggggctgca tctggcttgg     1543

tggtagcatt taatctattg cattggtgtt tttcagatga aagagaaatc catataccat     1603

tatgtttgaa tttcctgata tatacaggat ttaaagtgaa aactttattc caagagttaa     1663

cagagtctct gggaagcttt aggacatctg ctacgttatt tatcaaaata ttgggatctc     1723

tgccttgtgc ctacagtgtc gtgggcctgc tcgctagcag aagtcagaaa aggcgatagg     1783

cttggcttta aggatttcgt gcccttgcct gaattcagta caactccact gcctcacgtt     1843

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1               5               10              15
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         20              25              30

Ala Leu Val Leu Lys Pro Gln Met Leu Lys Gly Glu Leu Gln Thr Arg
         35              40              45

Pro Ser Gln Arg Pro Ser Arg Lys Ala Phe Arg Arg Asn Asn Phe Glu
    50              55              60

Tyr Thr Leu Glu Ala Ser Lys Ser Leu Arg Gln Lys Pro Gly Asp Ser
65              70              75              80

Thr Met Thr Tyr Leu Asn Lys Gly Gln Phe Tyr Pro Ile Thr Leu Lys
             85              90              95

Glu Val Ser Ser Ser Glu Gly Ile His His Pro Ile Ser Lys Val Arg
             100             105             110

Ser Val Ile Met Val Val Phe Ala Glu Asp Lys Ser Arg Glu Asp Gln
             115             120             125

Leu Arg His Trp Lys Tyr Trp His Ser Arg Gln His Thr Ala Lys Gln
    130             135             140

Arg Cys Ile Asp Ile Ala Asp Tyr Lys Glu Ser Phe Asn Thr Ile Ser
145             150             155             160

Asn Ile Glu Glu Ile Ala Tyr Asn Ala Ile Ser Phe Thr Trp Asp Ile
             165             170             175

Asn Asp Glu Ala Lys Val Phe Ile Ser Val Asn Cys Leu Ser Thr Asp
             180             185             190

Phe Ser Ser Gln Lys Gly Val Lys Gly Leu Pro Leu Asn Ile Gln Val
             195             200             205

Asp Thr Tyr Ser Tyr Asn Asn Arg Ser Asn Lys Pro Val His Arg Ala
    210             215             220

Tyr Cys Gln Ile Lys Val Phe Cys Asp Lys Gly Ala Glu Arg Lys Ile
225             230             235             240
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- 5 -

Arg Asp Glu Glu Arg Lys Gln Ser Lys Arg Lys Val Ser Asp Val Lys
                245   250   255

Val Pro Leu Leu Pro Ser His Lys Arg Met Asp Ile Thr Val Phe Lys
                260   265   270

Pro Phe Ile Asp Leu Asp Thr Gln Pro Val Leu Phe Ile Pro Asp Val
                275   280   285

His Phe Ala Asn Leu Gln Arg Gly Thr His Val Leu Pro Ile Ala Ser
        290   295   300

Glu Glu Leu Glu Gly Glu Gly Ser Val Leu Lys Arg Gly Pro Tyr Gly
305   310   315   320

Thr Glu Asp Asp Phe Ala Val Pro Pro Ser Thr Lys Leu Ala Arg Ile
                325   330   335

Glu Glu Pro Lys Arg Val Leu Leu Tyr Val Arg Lys Glu Ser Glu Glu
                340   345   350

Val Phe Asp Ala Leu Met Leu Lys Thr Pro Ser Leu Lys Gly Leu Met
                355   360   365

Glu Ala Ile Ser Asp Lys Tyr Asp Val Pro His Asp Lys Ile Gly Lys
        370   375   380

Ile Phe Lys Lys Cys Lys Lys Gly Ile Leu Val Asn Met Asp Asp Asn
385   390   395   400

Ile Val Lys His Tyr Ser Asn Glu Asp Thr
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       1                 5                   10

cag aat gaa gca ctt tat cca cag cgg cgg tcc tac act agt gag gat      96
Gln Asn Glu Ala Leu Tyr Pro Gln Arg Arg Ser Tyr Thr Ser Glu Asp
15                  20                  25                  30

gag gcc tgg aaa tcc ttc ctg gaa aac cct ctc act gca gcg acc aaa     144
Glu Ala Trp Lys Ser Phe Leu Glu Asn Pro Leu Thr Ala Ala Thr Lys
                35                  40                  45

gcg atg atg agc atc aat gga gat gaa gac agc gcc gct gcg ctg ggc     192
Ala Met Met Ser Ile Asn Gly Asp Glu Asp Ser Ala Ala Ala Leu Gly
                50                  55                  60

ctg ctc tat gac tac tac aag gtt cca aga gag aga agg tca tca aca     240
Leu Leu Tyr Asp Tyr Tyr Lys Val Pro Arg Glu Arg Arg Ser Ser Thr
            65                  70                  75

gca aag cca gag gtg gag cac cct gag cca gat cac agc aaa aga aac     288.
Ala Lys Pro Glu Val Glu His Pro Glu Pro Asp His Ser Lys Arg Asn
        80                  85                  90

agc ata cca att gtg aca gag cag ccc ctc atc tct gct gga gaa aac     336
Ser Ile Pro Ile Val Thr Glu Gln Pro Leu Ile Ser Ala Gly Glu Asn
95                  100                 105                 110

aga gtg caa gta ctg aaa aat gtg cca ttt aac att gtc ctt ccc cat     384
Arg Val Gln Val Leu Lys Asn Val Pro Phe Asn Ile Val Leu Pro His
                115                 120                 125

ggc aac cag ctg ggc att gat aag aga ggc cat ctg aca gct tca gat     432
Gly Asn Gln Leu Gly Ile Asp Lys Arg Gly His Leu Thr Ala Ser Asp
            130                 135                 140

acg aca gtc act gtc tcc ata gca acg atg cct acc cac tcc atc aag     480
Thr Thr Val Thr Val Ser Ile Ala Thr Met Pro Thr His Ser Ile Lys
            145                 150                 155

aca gaa acc cag cca cat ggc ttc gct gtg gga atc ccc cca gca gtg     528
Thr Glu Thr Gln Pro His Gly Phe Ala Val Gly Ile Pro Pro Ala Val
        160                 165                 170

tat cat cct gag ccc act gag cgg gtg gtg gtt ttc gat cgg aay ctc     576
Tyr His Pro Glu Pro Thr Glu Arg Val Val Val Phe Asp Arg Asn Leu
175                 180                 185                 190

aat act gac cag ttc agc tct ggt gct caa gcc cca aat gct caa agg     624
Asn Thr Asp Gln Phe Ser Ser Gly Ala Gln Ala Pro Asn Ala Gln Arg
                195                 200                 205

cga act cca gac tcg acc ttc tca gag acc ttc aag gaa ggc gtt cag     672
Arg Thr Pro Asp Ser Thr Phe Ser Glu Thr Phe Lys Glu Gly Val Gln
        210                 215                 220

gag gtt ttc ttc ccc tcg gat ctc agt ctg cgg atg cct ggc atg aat     720
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- 7 -

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Glu Val Phe Phe Pro Ser Asp Leu Ser Leu Arg Met Pro Gly Met Asn
        225                 230                 235

tca gag gac tat gtt ttt gac agt gtt tct ggg aac aac ttt gaa tat        768
Ser Glu Asp Tyr Val Phe Asp Ser Val Ser Gly Asn Asn Phe Glu Tyr
    240                 245                 250

acc cta gaa gct tca aaa tca ctt cga cag aag cca gga gac agt acc        816
Thr Leu Glu Ala Ser Lys Ser Leu Arg Gln Lys Pro Gly Asp Ser Thr
255                 260                 265                 270

atg acg tac ctg aac aaa ggc cag ttc tat ccc atc acc ttg aag gag        864
Met Thr Tyr Leu Asn Lys Gly Gln Phe Tyr Pro Ile Thr Leu Lys Glu
                275                 280                 285

gtg agc agc agt gaa gga atc cat cat ccc atc agc aaa gtt cga agt        912
Val Ser Ser Ser Glu Gly Ile His His Pro Ile Ser Lys Val Arg Ser
            290                 295                 300

gtg atc atg gtg gtt ttt gct gaa gac aaa agc aga gaa gat cag tta        960
Val Ile Met Val Val Phe Ala Glu Asp Lys Ser Arg Glu Asp Gln Leu
        305                 310                 315

agg cat tgg aag tac tgg cac tcc cgg cag cac acc gct aaa caa aga      1008
Arg His Trp Lys Tyr Trp His Ser Arg Gln His Thr Ala Lys Gln Arg
    320                 325                 330

tgc att gac ata gct gac tat awa gaa agc ttc aac act atc agt aac      1056
Cys Ile Asp Ile Ala Asp Tyr Xaa Glu Ser Phe Asn Thr Ile Ser Asn
335                 340                 345                 350

atc gag gag att gcg tat aac gcc att tcc ttc aca tgg gac atc aac      1104
Ile Glu Glu Ile Ala Tyr Asn Ala Ile Ser Phe Thr Trp Asp Ile Asn
                355                 360                 365

gat gaa gca aag gtt ttc atc tct gtg aac tgc tta agc aca gat ttc      1152
Asp Glu Ala Lys Val Phe Ile Ser Val Asn Cys Leu Ser Thr Asp Phe
            370                 375                 380

tct tcc cag aag gga gtg aag ggg ttg cct ctt aac att caa gtt gat      1200
Ser Ser Gln Lys Gly Val Lys Gly Leu Pro Leu Asn Ile Gln Val Asp
        385                 390                 395

acc tat agt tac aac aac cgc agc aac aag cct gtg cac cgg gcc tac      1248
Thr Tyr Ser Tyr Asn Asn Arg Ser Asn Lys Pro Val His Arg Ala Tyr
    400                 405                 410

tgc cag atc aag gtc ttc tgt gac aag gga gct gag cgg aaa atc agg      1296
Cys Gln Ile Lys Val Phe Cys Asp Lys Gly Ala Glu Arg Lys Ile Arg
415                 420                 425                 430

gat gaa gaa cga aag caa agc aaa aga aaa gtt tct gat gtt aaa gtg      1344
Asp Glu Glu Arg Lys Gln Ser Lys Arg Lys Val Ser Asp Val Lys Val
            435                 440                 445

cca ctg ctt ccc tct cac aag cga atg gat atc aca gtt ttc aaa ccc      1392
Pro Leu Leu Pro Ser His Lys Arg Met Asp Ile Thr Val Phe Lys Pro
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- 8 -

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ttc att gat ctc gat act cag cct gtc ctc ttc att cct gac gtg cac        1440
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        465                    470                    475

ttt gcc aac ttg cag cgg ggc act cat gtc ctt ccc att gcc tct gaa        1488
Phe Ala Asn Leu Gln Arg Gly Thr His Val Leu Pro Ile Ala Ser Glu
        480                    485                    490

gaa ttg gag ggt gaa ggc tct gtc ttg aaa agg ggg ccg tac ggc aca        1536
Glu Leu Glu Gly Glu Gly Ser Val Leu Lys Arg Gly Pro Tyr Gly Thr
495                    500                    505                    510

gaa gat gac ttt gct gtc cct cct tct acc aag ctg gcc cgg ata gaa        1584
Glu Asp Asp Phe Ala Val Pro Pro Ser Thr Lys Leu Ala Arg Ile Glu
                515                    520                    525

gaa cca aag aga gtg ctg ctc tac gtt cga aag gag tca gaa gaa gtc        1632
Glu Pro Lys Arg Val Leu Leu Tyr Val Arg Lys Glu Ser Glu Glu Val
                530                    535                    540

ttt gat gcc ctg atg ctc aaa acc cca tct ttg aag ggc ttg atg gaa        1680
Phe Asp Ala Leu Met Leu Lys Thr Pro Ser Leu Lys Gly Leu Met Glu
                545                    550                    555

gct atc tca gac aaa tac gat gtt ccc cat gac aag att ggg aaa ata        1728
Ala Ile Ser Asp Lys Tyr Asp Val Pro His Asp Lys Ile Gly Lys Ile
        560                    565                    570

ttc aag aag tgt aaa aag ggg atc ctg gtg aac atg gac gac aac att        1776
Phe Lys Lys Cys Lys Lys Gly Ile Leu Val Asn Met Asp Asp Asn Ile
575                    580                    585                    590

gtg aag cat tac tcc aat gag gac acc ttc cag ctg cag att gaa gaa        1824
Val Lys His Tyr Ser Asn Glu Asp Thr Phe Gln Leu Gln Ile Glu Glu
                595                    600                    605

gcc ggg ggg tct tac aag ctc acc ctg acg gag atc taaaggcctg            1870
Ala Gly Gly Ser Tyr Lys Leu Thr Leu Thr Glu Ile
                610                    615


cgggccacag ctccccagga gttcagtgca ggtgtttcta gatcttacgg tttggcaact      1930

gcaggtaacc ccagtcagcc atgtcgccag cacaggtcta tgtcgaggga atgggttcct      1990

tgcaggttgg aggcggggct gcatctggct tggtggtagc atttaatcta ttgcattggt      2050

gtttttcaga tgaaagagaa atccatatac cattatgttt gaatttcctg atatatacag      2110

gatttaaagt gaaaacttta ttccaagagt taacagagtc tctgggaagc tttaggacat      2170

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-9-

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Trp Lys Ser Phe Leu Glu Asn Pro Leu Thr Ala Ala Thr Lys Ala Met
        35   40   45

Met Ser Ile Asn Gly Asp Glu Asp Ser Ala Ala Ala Leu Gly Leu Leu
    50   55   60

Tyr Asp Tyr Tyr Lys Val Pro Arg Glu Arg Arg Ser Ser Thr Ala Lys
65   70   75   80

Pro Glu Val Glu His Pro Glu Pro Asp His Ser Lys Arg Asn Ser Ile
                85   90   95

Pro Ile Val Thr Glu Gln Pro Leu Ile Ser Ala Gly Glu Asn Arg Val
            100   105   110

Gln Val Leu Lys Asn Val Pro Phe Asn Ile Val Leu Pro His Gly Asn
        115   120   125

Gln Leu Gly Ile Asp Lys Arg Gly His Leu Thr Ala Ser Asp Thr Thr
    130   135   140

Val Thr Val Ser Ile Ala Thr Met Pro Thr His Ser Ile Lys Thr Glu
145   150   155   160

Thr Gln Pro His Gly Phe Ala Val Gly Ile Pro Pro Ala Val Tyr His

- 10 -

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                 165                    170                    175


   Pro Glu Pro Thr Glu Arg Val Val Val Phe Asp Arg Asn Leu Asn Thr
               180                185                190


   Asp Gln Phe Ser Ser Gly Ala Gln Ala Pro Asn Ala Gln Arg Arg Thr
               195                200                205


   Pro Asp Ser Thr Phe Ser Glu Thr Phe Lys Glu Gly Val Gln Glu Val
       210                215                220


   Phe Phe Pro Ser Asp Leu Ser Leu Arg Met Pro Gly Met Asn Ser Glu
   225                230                235                240


   Asp Tyr Val Phe Asp Ser Val Ser Gly Asn Asn Phe Glu Tyr Thr Leu
               245                250                255


   Glu Ala Ser Lys Ser Leu Arg Gln Lys Pro Gly Asp Ser Thr Met Thr
               260                265                270


   Tyr Leu Asn Lys Gly Gln Phe Tyr Pro Ile Thr Leu Lys Glu Val Ser
               275                280                285


   Ser Ser Glu Gly Ile His His Pro Ile Ser Lys Val Arg Ser Val Ile
       290                295                300


   Met Val Val Phe Ala Glu Asp Lys Ser Arg Glu Asp Gln Leu Arg His
   305                310                315                320


   Trp Lys Tyr Trp His Ser Arg Gln His Thr Ala Lys Gln Arg Cys Ile
               325                330                335


   Asp Ile Ala Asp Tyr Xaa Glu Ser Phe Asn Thr Ile Ser Asn Ile Glu
               340                345                350


   Glu Ile Ala Tyr Asn Ala Ile Ser Phe Thr Trp Asp Ile Asn Asp Glu
               355                360                365


   Ala Lys Val Phe Ile Ser Val Asn Cys Leu Ser Thr Asp Phe Ser Ser
       370                375                380


   Gln Lys Gly Val Lys Gly Leu Pro Leu Asn Ile Gln Val Asp Thr Tyr
   385                390                395                400
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- 11 -

Ser Tyr Asn Asn Arg Ser Asn Lys Pro Val His Arg Ala Tyr Cys Gln
            405   410   .   415

Ile Lys Val Phe Cys Asp Lys Gly Ala Glu Arg Lys Ile Arg Asp Glu
        .   420   425   430

Glu Arg Lys Gln Ser Lys Arg Lys Val Ser Asp Val Lys Val Pro Leu
        435   440   ∞   445

Leu Pro Ser His Lys Arg Met Asp Ile Thr Val Phe Lys Pro Phe Ile
        450   455   .   460

Asp Leu Asp Thr Gln Pro Val Leu Phe Ile Pro Asp Val His Phe Ala
465   470   475   480

Asn Leu Gln Arg Gly Thr His Val Leu Pro Ile Ala Ser Glu Glu Leu
            485   490   .   495

Glu Gly Glu Gly Ser Val Leu Lys Arg Gly Pro Tyr Gly Thr Glu Asp
            500   505   510

Asp Phe Ala Val Pro Pro Ser Thr Lys Leu Ala Arg Ile Glu Glu Pro
            515   520   .   .   525

Lys Arg Val Leu Leu Tyr Val Arg Lys Glu Ser Glu Glu Val Phe Asp
            530   535   .   540

Ala Leu Met Leu Lys Thr Pro Ser Leu Lys Gly Leu Met Glu Ala Ile
545   550   .   555   .   560

Ser Asp Lys Tyr Asp Val Pro His Asp Lys Ile Gly Lys Ile Phe Lys
            565   .   570   575

Lys Cys Lys Lys Gly Ile Leu Val Asn Met Asp Asp Asn Ile Val Lys
            580   585   590

His Tyr Ser Asn Glu Asp Thr Phe Gln Leu Gln Ile Glu Glu Ala Gly
            595   600   605

Gly Ser Tyr Lys Leu Thr Leu Thr Glu Ile
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       Met Ser Gln Glu Ser Asp Asn Asn Lys Arg Leu Val Ala Leu
        1   5   10

gtg ccc atg ccc agt gac cct cca ttc aat acc cga aga gcc tac acc   156
Val Pro Met Pro Ser Asp Pro Pro Phe Asn Thr Arg Arg Ala Tyr Thr
15   20   25   30

agt gag gat gaa gcc tgg aag tca tac ttg gag aat ccc ctg aca gca   204
Ser Glu Asp Glu Ala Trp Lys Ser Tyr Leu Glu Asn Pro Leu Thr Ala
                35   40   45

gcc acc aag gcc atg atg agc att aat ggt gat gag gac agt gct gct   252
Ala Thr Lys Ala Met Met Ser Ile Asn Gly Asp Glu Asp Ser Ala Ala
            50   55   60

gcc ctc ggc ctg ctc tat gac tac tac aag gtt cct cga gac aag agg   300
Ala Leu Gly Leu Leu Tyr Asp Tyr Tyr Lys Val Pro Arg Asp Lys Arg
            65   70   75

ctg ctg tct gta agc aaa gca agt gac agc caa gaa gac cag gag aaa   348
Leu Leu Ser Val Ser Lys Ala Ser Asp Ser Gln Glu Asp Gln Glu Lys
        80   85   90

aga aac tgc ctt ggc acc agt gaa gcc cag agt aat ttg agt gga gga   396
Arg Asn Cys Leu Gly Thr Ser Glu Ala Gln Ser Asn Leu Ser Gly Gly
95   100   105   110

gaa aac cga gtg caa gtc cta aag act gtt cca gtg aac ctt tcc cta   444
Glu Asn Arg Val Gln Val Leu Lys Thr Val Pro Val Asn Leu Ser Leu
                115   120   125

aat caa gat cac ctg gag aat tcc aag cgg gaa cag tac agc atc agc   492
Asn Gln Asp His Leu Glu Asn Ser Lys Arg Glu Gln Tyr Ser Ile Ser
            130   135   140

ttc ccc gag agc tct gcc atc atc ccg gtg tcg gga atc acg gtg gtg   540
Phe Pro Glu Ser Ser Ala Ile Ile Pro Val Ser Gly Ile Thr Val Val
            145   150   155

aaa gct gaa gat ttc aca cca gtt ttc atg gcc cca cct gtg cac tat   588
Lys Ala Glu Asp Phe Thr Pro Val Phe Met Ala Pro Pro Val His Tyr

- 13 -

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         160                    165                    170

ccc cgg gga gat ggg gaa gag caa cga gtg gtt atc ttt gaa cag act          636
Pro Arg Gly Asp Gly Glu Glu Gln Arg Val Val Ile Phe Glu Gln Thr
175             180              ·185                190

cag tat gac gtg ccc tcg ctg gcc acc cac agc gcc tat ctc aaa gac          684
Gln Tyr Asp Val Pro Ser Leu Ala Thr His Ser Ala Tyr Leu Lys Asp
                195              200              205

gac cag cgc agc act ccg gac agc aca tac agc gag agc ttc aag gac          732
Asp Gln Arg Ser Thr Pro Asp Ser Thr Tyr Ser Glu Ser Phe Lys Asp
                210              215              220

gca gcc aca gag aaa ttt cgg agt gct tca gtt ggg gct gag gag tac          780
Ala Ala Thr Glu Lys Phe Arg Ser Ala Ser Val Gly Ala Glu Glu Tyr
                225              230              235

atg tat gat cag aca tca agt ggc aca ttt cag tac acc ctg gaa gcc          828
Met Tyr Asp Gln Thr Ser Ser Gly Thr Phe Gln Tyr Thr Leu Glu Ala
                240              245              250

acc aaa tct ctc cgt cag aag cag ggg gag ggc ccc atg acc tac ctc          876
Thr Lys Ser Leu Arg Gln Lys Gln Gly Glu Gly Pro Met Thr Tyr Leu
255             260              265              270

aac aaa gga cag ttc tat gcc ata aca ctc agc gag acc gga gac aac          924
Asn Lys Gly Gln Phe Tyr Ala Ile Thr Leu Ser Glu Thr Gly Asp Asn
                275              280              285

aaa tgc ttc cga cac ccc atc agc aaa gtc agg agt gtg gtg atg gtg          972
Lys Cys Phe Arg His Pro Ile Ser Lys Val Arg Ser Val Val Met Val
                290              295              300

gtc ttc agt gaa gac aaa aac aga gat gaa cag ctc aaa tac tgg aaa          1020
Val Phe Ser Glu Asp Lys Asn Arg Asp Glu Gln Leu Lys Tyr Trp Lys
                305              310              315

tac tgg cac tct cgg cag cat acg gcg aag cag agg gtc ctt gac att          1068
Tyr Trp His Ser Arg Gln His Thr Ala Lys Gln Arg Val Leu Asp Ile
                320              325              330

gcc gat tac aag gag agc ttt aat acg att gga aac att gaa gag att          1116
Ala Asp Tyr Lys Glu Ser Phe Asn Thr Ile Gly Asn Ile Glu Glu Ile
335             340              345              350

gca tat aat gct gtt tcc ttt acc tgg gac gtg aat gaa gag gcg aag          1164
Ala Tyr Asn Ala Val Ser Phe Thr Trp Asp Val Asn Glu Glu Ala Lys
                355              360              365

att ttc atc acc gtg aat tgc ttg agc aca gat ttc tcc tcc caa aaa          1212
Ile Phe Ile Thr Val Asn Cys Leu Ser Thr Asp Phe Ser Ser Gln Lys
                370              375              380

ggg gtg aaa gga ctt cct ttg atg att cag att gac aca tac agt tat          1260
Gly Val Lys Gly Leu Pro Leu Met Ile Gln Ile Asp Thr Tyr Ser Tyr
                385              390              395
```

- 14 -

```
aac aat cgt agc aat aaa ccc att cat aga gct tat tgc cag atc aag      1308
Asn Asn Arg Ser Asn Lys Pro Ile His Arg Ala Tyr Cys Gln Ile Lys
    400                 405                 410

gtc ttc tgt gac aaa gga gca gaa aga aaa atc cga gat gaa gag cgg      1356
Val Phe Cys Asp Lys Gly Ala Glu Arg Lys Ile Arg Asp Glu Glu Arg
415                 420                 425                 430

aag cag aac agg aag aaa ggg aaa ggc cag gcc tcc caa act caa tgc      1404
Lys Gln Asn Arg Lys Lys Gly Lys Gly Gln Ala Ser Gln Thr Gln Cys
                435                 440                 445

aac agc tcc tct gat ggg aag ttg gct gcc ata cct tta cag aag aag      1452
Asn Ser Ser Ser Asp Gly Lys Leu Ala Ala Ile Pro Leu Gln Lys Lys
            450                 455                 460

agt gac atc acc tac ttc aaa acc atg cct gat ctc cac tca cag cca      1500
Ser Asp Ile Thr Tyr Phe Lys Thr Met Pro Asp Leu His Ser Gln Pro
            465                 470                 475

gtt ctc ttc ata cct gat gtt cac ttt gca aac ctg cag agg acc gga      1548
Val Leu Phe Ile Pro Asp Val His Phe Ala Asn Leu Gln Arg Thr Gly
    480                 485                 490

cag gtg tat tac aac acg gat gat gaa cga gaa ggt ggc agt gtc ctt      1596
Gln Val Tyr Tyr Asn Thr Asp Asp Glu Arg Glu Gly Gly Ser Val Leu
495                 500                 505                 510

gtt aaa cgg atg ttc cgg ccc atg gaa gag gag ttt ggt cca gtg cct      1644
Val Lys Arg Met Phe Arg Pro Met Glu Glu Glu Phe Gly Pro Val Pro
                515                 520                 525

tca aag cag atg aaa gaa gaa ggg aca aag cga gtg ctc ttg tac gtg      1692
Ser Lys Gln Met Lys Glu Glu Gly Thr Lys Arg Val Leu Leu Tyr Val
                530                 535                 540

agg aag gag act gac gat gtg ttc gat gca ttg atg ttg aag tct ccc      1740
Arg Lys Glu Thr Asp Asp Val Phe Asp Ala Leu Met Leu Lys Ser Pro
            545                 550                 555

aca gtg aag ggc ctg atg gaa gcg ata tct gag aaa tat ggg ctg ccc      1788
Thr Val Lys Gly Leu Met Glu Ala Ile Ser Glu Lys Tyr Gly Leu Pro
    560                 565                 570

gtg gag aag ata gca aag ctt tac aag aaa agc aaa aaa ggc atc ttg      1836
Val Glu Lys Ile Ala Lys Leu Tyr Lys Lys Ser Lys Lys Gly Ile Leu
575                 580                 585                 590

gtg aac atg gat gac aac atc atc gag cac tac tcg aac gag gac acc      1884
Val Asn Met Asp Asp Asn Ile Ile Glu His Tyr Ser Asn Glu Asp Thr
                595                 600                 605

ttc atc ctc aac atg gag agc atg gtg gag ggc ttc aag gtc acg ctc      1932
Phe Ile Leu Asn Met Glu Ser Met Val Glu Gly Phe Lys Val Thr Leu
                610                 615                 620
```

- 15 -

```
atg gaa atc tagccctggg tttggcatcc gctttggctg gagctctcag              1981
Met Glu Ile
        625

tgcgttcctc cctgagagag acagaagccc cagccccaga acctggagac ccatctcccc    2041

catctcacaa ctgctgttac aagaccgtgc tggggagtgg ggcaagggac aggccccact    2101

gtcggtgtgc ttggcccatc cactggcacc taccacggag ctgaagcctg agcccctcag    2161

gaaggtgcct taggcctgtt ggattcctat ttattgccca ccttttcctg gagcccaggt    2221

ccaggcccgc caggactctg caggtcactg ctagctccag atgagaccgt ccagcgttcc    2281

cccttcaaga gaaacactca tcccgaacag cctaaaaaat tcccatccct tctctctcac    2341

ccctccatat ctatctcccg agtggctgga caaaatgagc tacgtctggg tgcagtagtt    2401

ataggtgggg caagaggtgg atgcccactt tctggtcaga cacctttagg ttgctctggg    2461

gaaggctgtc ttgctaaata cctccagggt tcccagcaag tggccaccag gccttgtaca    2521

ggaagacatt cagtcaccgt gtaattagta acacagaaag tctgcctgtc tgcattgtac    2581

atagtgttta taatattgta ataatatatt ttacctgtgg tatgtgggca tgtttactgc    2641

cactggcctt agaggagaca cagacctgga daccgtttta atgggggttt ttgcctctgt    2701

gcctgttcaa gagacttgca gggctaggta gagggccttt gggatgttaa ggtgactgca    2761

gctgatgcca agatggactc tgcaatgggc atacctgggg gctcgttccc tgtccccaga    2821

ggaagccccc tctccttctc catgggcatg actctccttc gaggccacca cgtttatctc    2881

acaatgatgt gttttgcttg actttccctt tgcgctgtct cgtgggaaag gtcattctgt    2941

ctgagacccc agctccttct ccagctttgg ctgcgggcat ggcctgagct ttctggagag    3001

cctctgcagg gggtttgcca tcagggccct gtggctgggt ctgctgcaga gctccttggc    3061

tatcaggaga atcctggaca ctgtactgtg cctcccagtt tacaaacacg cccttcatct    3121

caagtggccc tttaaaaggc ctgctgccat gtgagagctg tgaacagctc agctctgagt    3181

cggcaggctg gggcttcctc ctgggccacc agatggaaag ggggtattgt ttgcctcact    3241

cctggatgct gcgttttaag gaagtgagtg agaaagaatg tgccaagata cctggctcct    3301

gtgaaaccag cctcaggagg gaaactggga gagagaagct gtggtctcct gctacatgcc    3361

ctgggagctg gaagagaaaa acactcccct aaacaatcgc aaaatgatga accatcatgg    3421

gccactgttc tctttgaggg gacaggttta ggggtttgcg ttcgcccttg tgggctgaag    3481

cactagcttt ttggtagcta gacacatcct gcacccaaag gttctctaca aaggcccaga    3541

tttgtttgta aagcactttg actcttacct ggaggcccgc tctctaaggg cttcctgcgc    3601
```

- 16 -

```
tcccacctca tctgtccctg agatgcagag caggatggag ggtctgcttc tagctcagct   3661

gtttctcctt gaggttgcgg aggaattgaa ttgaatggga cagagggcag gtgctgtggc   3721

caagaagatc tccgagcagc agtgacgggg caccttgctg tgtgtcctct gggcatgtta   3781

acccttctgt ggggccaaag gtttgcatcg tggatccagc tgtgctccag tctgtcccct   3841

cctcctccac tctgactgcc acgccccgga ccagcagctt ggggaccctc agggtacta    3901

atggggctct gttctgagat ggacaaattc agtgttggaa atacatgttg tactatgcac   3961

ttcccatgct cctagggtta ggaatagttt caaacatgat tggcagacat aacaacggca   4021

aatactcgga ctggggcata ggactccaga gtaggaaaaa gacaaagat ttggcagcct    4081

gacacaggca acctacccct ctctctccag cctctttatg aaactgtttg tttgccagtc   4141

ctgccctaag gcagaagatg aattgaagat gctgtgcatg tttcctaagt ccttgagcaa   4201

tcatggtggt gacaattgcc acaagggata tgaggccagt gccaccagag ggtggtgcca   4261

agtgccacat cccttccgat ccattcccct ctgcatcctc ggagcacccc agtttgcctt   4321

tgatgtgtcc gctgtgtatg ttagctgaac tttgatgagc aaaatttcct gagcgaaaca   4381

ctccaaagag ataggaaaac ttgccgcctc ttcttttttg tcccttaatc aaactcaaat    4441

aagcttaaaa aaaatccatg gaagatcatg gacatgtgaa atgagcattt ttttcttttt   4501

tttttttttt tttaacaaag tctgaactga g                                   4532
```

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<212>   PRT
<213>   human

<400>   6

Met Ser Gln Glu Ser Asp Asn Asn Lys Arg Leu Val Ala Leu Val Pro
1               5                   10                  15


Met Pro Ser Asp Pro Pro Phe Asn Thr Arg Arg Ala Tyr Thr Ser Glu
            20                  25                  30


Asp Glu Ala Trp Lys Ser Tyr Leu Glu Asn Pro Leu Thr Ala Ala Thr
        35                  40                  45


Lys Ala Met Met Ser Ile Asn Gly Asp Glu Asp Ser Ala Ala Ala Leu
    50                  55                  60
```

- 17 -

Gly Leu Leu Tyr Asp Tyr Tyr Lys Val Pro Arg Asp Lys Arg Leu Leu
65   70   75   80

Ser Val Ser Lys Ala Ser Asp Ser Gln Glu Asp Gln Glu Lys Arg Asn
                    85   90   95

Cys Leu Gly Thr Ser Glu Ala Gln Ser Asn Leu Ser Gly Gly Glu Asn
                100   105   110

Arg Val Gln Val Leu Lys Thr Val Pro Val Asn Leu Ser Leu Asn Gln
        115   120   125

Asp His Leu Glu Asn Ser Lys Arg Glu Gln Tyr Ser Ile Ser Phe Pro
    130   135   140

Glu Ser Ser Ala Ile Ile Pro Val Ser Gly Ile Thr Val Val Lys Ala
145   150   155   160

Glu Asp Phe Thr Pro Val Phe Met Ala Pro Pro Val His Tyr Pro Arg
                165   170   175

Gly Asp Gly Glu Glu Gln Arg Val Val Ile Phe Glu Gln Thr Gln Tyr
                180   185   190

Asp Val Pro Ser Leu Ala Thr His Ser Ala Tyr Leu Lys Asp Asp Gln
        195   200   205

Arg Ser Thr Pro Asp Ser Thr Tyr Ser Glu Ser Phe Lys Asp Ala Ala
    210   215   220

Thr Glu Lys Phe Arg Ser Ala Ser Val Gly Ala Glu Glu Tyr Met Tyr
225   230   235   240

Asp Gln Thr Ser Ser Gly Thr Phe Gln Tyr Thr Leu Glu Ala Thr Lys
                245   250   255

Ser Leu Arg Gln Lys Gln Gly Glu Gly Pro Met Thr Tyr Leu Asn Lys
            260   265   270

Gly Gln Phe Tyr Ala Ile Thr Leu Ser Glu Thr Gly Asp Asn Lys Cys
        275   280   285

Phe Arg His Pro Ile Ser Lys Val Arg Ser Val Val Met Val Val Phe

- 18 -

```
        290                    295                    300

Ser Glu Asp Lys Asn Arg Asp Glu Gln Leu Lys Tyr Trp Lys Tyr Trp
305                 310                 315                 320

His Ser Arg Gln His Thr Ala Lys Gln Arg Val Leu Asp Ile Ala Asp
                325                 330                 335

Tyr Lys Glu Ser Phe Asn Thr Ile Gly Asn Ile Glu Glu Ile Ala Tyr
            340                 345                 350

Asn Ala Val Ser Phe Thr Trp Asp Val Asn Glu Glu Ala Lys Ile Phe
            355                 360                 365

Ile Thr Val Asn Cys Leu Ser Thr Asp Phe Ser Ser Gln Lys Gly Val
    370                 375                 380

Lys Gly Leu Pro Leu Met Ile Gln Ile Asp Thr Tyr Ser Tyr Asn Asn
385                 390                 395                 400

Arg Ser Asn Lys Pro Ile His Arg Ala Tyr Cys Gln Ile Lys Val Phe
                405                 410                 415

Cys Asp Lys Gly Ala Glu Arg Lys Ile Arg Asp Glu Glu Arg Lys Gln
            420                 425                 430

Asn Arg Lys Lys Gly Lys Gly Gln Ala Ser Gln Thr Gln Cys Asn Ser
            435                 440                 445

Ser Ser Asp Gly Lys Leu Ala Ala Ile Pro Leu Gln Lys Lys Ser Asp
    450                 455                 460

Ile Thr Tyr Phe Lys Thr Met Pro Asp Leu His Ser Gln Pro Val Leu
465                 470                 475                 480

Phe Ile Pro Asp Val His Phe Ala Asn Leu Gln Arg Thr Gly Gln Val
                485                 490                 495

Tyr Tyr Asn Thr Asp Asp Glu Arg Glu Gly Gly Ser Val Leu Val Lys
            500                 505                 510

Arg Met Phe Arg Pro Met Glu Glu Glu Phe Gly Pro Val Pro Ser Lys
        515                 520                 525
```

- 19 -

```
Gln Met Lys Glu Glu Gly Thr Lys Arg Val Leu Leu Tyr Val Arg Lys
    530             535             540

Glu Thr Asp Asp Val Phe Asp Ala Leu Met Leu Lys Ser Pro Thr Val
545             550             555             560

Lys Gly Leu Met Glu Ala Ile Ser Glu Lys Tyr Gly Leu Pro Val Glu
                565             570             575

Lys Ile Ala Lys Leu Tyr Lys Lys Ser Lys Lys Gly Ile Leu Val Asn
            580             585             590

Met Asp Asp Asn Ile Ile Glu His Tyr Ser Asn Glu Asp Thr Phe Ile
        595             600             605

Leu Asn Met Glu Ser Met Val Glu Gly Phe Lys Val Thr Leu Met Glu
    610             615             620

Ile
625
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<210>   7
<211>   1870
<212>   DNA
<213>   HUMAN

<220>
<221>   CDS
<222>   (47)..(1867)
<223>

<400>   7
aggagatgtg ccaaactgtt aagagtggtt atttctgagc agaaga atg tgg atg        55
                                                   Met Trp Met
                                                    1

aat tcc att ctt cct att ttt ctt ttc agg tct gtg cgg ctg cta aag        103
Asn Ser Ile Leu Pro Ile Phe Leu Phe Arg Ser Val Arg Leu Leu Lys
    5               10              15

aac gac cca gtc aac ttg cag aaa ttc tct tac act agt gag gat gag        151
Asn Asp Pro Val Asn Leu Gln Lys Phe Ser Tyr Thr Ser Glu Asp Glu
20              25              30                  35

gcc tgg aag acg tac cta gaa aac ccg ttg aca gct gcc aca aag gcc        199
Ala Trp Lys Thr Tyr Leu Glu Asn Pro Leu Thr Ala Ala Thr Lys Ala
            40              45              50
```

- 20 -

```
atg atg aga gtc aat gga gat gat gac agt gtt gcg gcc ttg agc ttc      247
Met Met Arg Val Asn Gly Asp Asp Asp Ser Val Ala Ala Leu Ser Phe
            55              60                      65

ctc tat gat tac tac atg ggt ccc aag gag aag cgg ata ttg tcc tcc      295
Leu Tyr Asp Tyr Tyr Met Gly Pro Lys Glu Lys Arg Ile Leu Ser Ser
            70              75                      80

agc act ggg ggc agg aat gac caa gga aag agg tac tac cat ggc atg      343
Ser Thr Gly Gly Arg Asn Asp Gln Gly Lys Arg Tyr Tyr His Gly Met
        85              90                      95

gaa tat gag acg gac ctc act ccc ctt gaa agc ccc aca cac ctc atg      391
Glu Tyr Glu Thr Asp Leu Thr Pro Leu Glu Ser Pro Thr His Leu Met
100                 105                     110                 115

aaa ytc ctg aca gag aac gtg tct gga acc cca gag tac cca gat ttg      439
Lys Xaa Leu Thr Glu Asn Val Ser Gly Thr Pro Glu Tyr Pro Asp Leu
                    120                 125                 130

ctc aag aag aat aac ctg atg agc ttg gag ggg gcc ttg ccc acc cct      487
Leu Lys Lys Asn Asn Leu Met Ser Leu Glu Gly Ala Leu Pro Thr Pro
                135                 140                 145

ggc aag gca gct ccc ctc cct gca ggc ccc agc aag ctg gag gcc ggc      535
Gly Lys Ala Ala Pro Leu Pro Ala Gly Pro Ser Lys Leu Glu Ala Gly
        150                 155                 160

tct gtg gac agc tac ctg tta ccc acy act gat atg tat gat aat ggc      583
Ser Val Asp Ser Tyr Leu Leu Pro Xaa Thr Asp Met Tyr Asp Asn Gly
        165                 170                 175

tcc ctc aac tcc ttg ttt gag agc att cat ggg gtg ccg ccc aca cag      631
Ser Leu Asn Ser Leu Phe Glu Ser Ile His Gly Val Pro Pro Thr Gln
180                 185                 190                 195

cgc tgg cag cca gac agc acc ttc aaa gat gac cca cag gag tcg atg      679
Arg Trp Gln Pro Asp Ser Thr Phe Lys Asp Asp Pro Gln Glu Ser Met
                200                 205                 210

ctc ttc cca gat atc ctg aaa acc tcc ccg gaa ccc cca tgt cca gag      727
Leu Phe Pro Asp Ile Leu Lys Thr Ser Pro Glu Pro Pro Cys Pro Glu
                215                 220                 225

gac tac ccc agc ctc aaa agt gac ttt gaa tac acc ctg ggc tcc ccc      775
Asp Tyr Pro Ser Leu Lys Ser Asp Phe Glu Tyr Thr Leu Gly Ser Pro
            230                 235                 240

aaa gcc atc cac atc aag tca ggc gag tca ccc atg gcc tac ctc aac      823
Lys Ala Ile His Ile Lys Ser Gly Glu Ser Pro Met Ala Tyr Leu Asn
    245                 250                 255

aaa ggc cag ttc tac ccc gtc acc ctg cgg acc cca gca ggt ggc aaa      871
Lys Gly Gln Phe Tyr Pro Val Thr Leu Arg Thr Pro Ala Gly Gly Lys
260                 265                 270                 275
```

```
ggc ctt gcc ttg tcc tcc aac aaa gtc aag agt gtg gtg atg gtt gtc        919
Gly Leu Ala Leu Ser Ser Asn Lys Val Lys Ser Val Val Met Val Val
            280                 285                 290

ttc gac aat gag aag gtc cca gta gag cag ctg cgc ttc tgg aag cac        967
Phe Asp Asn Glu Lys Val Pro Val Glu Gln Leu Arg Phe Trp Lys His
            295                 300                 305

tgg cat tcc cgg caa ccc act gcc aag cag cgg gtc att gac gtg gct       1015
Trp His Ser Arg Gln Pro Thr Ala Lys Gln Arg Val Ile Asp Val Ala
            310                 315                 320

gac tgc aaa gaa aac ttc aac act gtg gag cac att gag gag gtg gcc       1063
Asp Cys Lys Glu Asn Phe Asn Thr Val Glu His Ile Glu Glu Val Ala
            325                 330                 335

tat aat gca ctg tcc ttt gtg tgg aac gtg aat gaa gag gcc aag gtg       1111
Tyr Asn Ala Leu Ser Phe Val Trp Asn Val Asn Glu Glu Ala Lys Val
340                 345                 350                 355

ttc atc ggc gta aac tgt ctg agc aca gac ttt tcc tca caa aag ggg       1159
Phe Ile Gly Val Asn Cys Leu Ser Thr Asp Phe Ser Ser Gln Lys Gly
                    360                 365                 370

gtg aag ggt gtc ccc ctg aac ctg cag att gac acc tat gac tgt ggc       1207
Val Lys Gly Val Pro Leu Asn Leu Gln Ile Asp Thr Tyr Asp Cys Gly
                    375                 380                 385

ttg ggc act gag cgc ctg gta cac cgt gct gtc tgc cag atc aag atc       1255
Leu Gly Thr Glu Arg Leu Val His Arg Ala Val Cys Gln Ile Lys Ile
            390                 395                 400

ttc tgt gac aag gga gct gag agg aag atg cgc gat gac gag cgg aag       1303
Phe Cys Asp Lys Gly Ala Glu Arg Lys Met Arg Asp Asp Glu Arg Lys
            405                 410                 415

cag ttc cgg agg aag gtc aag tgc cct gac tcc agc aac agt ggc gtc       1351
Gln Phe Arg Arg Lys Val Lys Cys Pro Asp Ser Ser Asn Ser Gly Val
420                 425                 430                 435

aag ggc tgc ctg ctg tcg ggc ttc agg ggc aat gag acg acc tac ctt       1399
Lys Gly Cys Leu Leu Ser Gly Phe Arg Gly Asn Glu Thr Thr Tyr Leu
                    440                 445                 450

cgg cca gag act gac ctg gag acg cca ccc gtg ctg ttc atc ccc aat       1447
Arg Pro Glu Thr Asp Leu Glu Thr Pro Pro Val Leu Phe Ile Pro Asn
            455                 460                 465

gtg cac ttc tcc agc ctg cag cgc tct gga ggg gca gcc ccc tcg gca       1495
Val His Phe Ser Ser Leu Gln Arg Ser Gly Gly Ala Ala Pro Ser Ala
            470                 475                 480

gga ccc agc agc tcc aac agg ctg cct ctg aag cgt acc tgc tcg ccc       1543
Gly Pro Ser Ser Ser Asn Arg Leu Pro Leu Lys Arg Thr Cys Ser Pro
485                 490                 495

ttc act gag gag ttt gag cct ctg ccc tcc aag cag gcc aag gaa ggc       1591
Phe Thr Glu Glu Phe Glu Pro Leu Pro Ser Lys Gln Ala Lys Glu Gly
```

- 22 -

```
Phe Thr Glu Glu Phe Glu Pro Leu Pro Ser Lys Gln Ala Lys Glu Gly
500             505             510             515


gac ctt cag aga gtt ctg ctg tat gtg cgg agg gag act gag gag gtg        1639
Asp Leu Gln Arg Val Leu Leu Tyr Val Arg Arg Glu Thr Glu Glu Val
            520             525             530


ttt gac gcg ctc atg ttg aag acc cca gac ctg aag ggg ctg agg aat        1687
Phe Asp Ala Leu Met Leu Lys Thr Pro Asp Leu Lys Gly Leu Arg Asn
            535             540             545


gcg atc tct gag aag tat ggg ttc cct gaa gag aac att tac aaa gtc        1735
Ala Ile Ser Glu Lys Tyr Gly Phe Pro Glu Glu Asn Ile Tyr Lys Val
            550             555             560


tac aag aaa tgc aag cga gga atc tta gtc aac atg gac aac aac atc        1783
Tyr Lys Lys Cys Lys Arg Gly Ile Leu Val Asn Met Asp Asn Asn Ile
            565             570             575


att cag cat tac agc aac cac gtc gcc ttc ctg ctg gac atg ggg gag        1831
Ile Gln His Tyr Ser Asn His Val Ala Phe Leu Leu Asp Met Gly Glu
580             585             590             595


ctg gac ggc aaa att cag atc atc ctt aag gag ctg taa                    1870
Leu Asp Gly Lys Ile Gln Ile Ile Leu Lys Glu Leu
            600             605
```

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<210>  8
<211>  607
<212>  PRT
<213>  HUMAN

<220>
<221>  misc_feature
<222>  (117)..(117)
<223>  The 'Xaa' at location 117 stands for Leu, or Phe.

<220>
<221>  misc_feature
<222>  (172)..(172)
<223>  The 'Xaa' at location 172 stands for Thr.

<400>  8
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```
Met Trp Met Asn Ser Ile Leu Pro Ile Phe Leu Phe Arg Ser Val Arg
1               5               10              15


Leu Leu Lys Asn Asp Pro Val Asn Leu Gln Lys Phe Ser Tyr Thr Ser
            20              25              30


Glu Asp Glu Ala Trp Lys Thr Tyr Leu Glu Asn Pro Leu Thr Ala Ala
            35              40              45
```

- 23 -

```
Thr Lys Ala Met Met Arg Val Asn Gly Asp Asp Asp Ser Val Ala Ala
    50              55              60

Leu Ser Phe Leu Tyr Asp Tyr Tyr Met Gly Pro Lys Glu Lys Arg Ile
65              70              75                  80

Leu Ser Ser Ser Thr Gly Gly Arg Asn Asp Gln Gly Lys Arg Tyr Tyr
                85              90                  95

His Gly Met Glu Tyr Glu Thr Asp Leu Thr Pro Leu Glu Ser Pro Thr
            100             105             110

His Leu Met Lys Xaa Leu Thr Glu Asn Val Ser Gly Thr Pro Glu Tyr
        115             120             125

Pro Asp Leu Leu Lys Lys Asn Asn Leu Met Ser Leu Glu Gly Ala Leu
    130             135             140

Pro Thr Pro Gly Lys Ala Ala Pro Leu Pro Ala Gly Pro Ser Lys Leu
145             150             155             160

Glu Ala Gly Ser Val Asp Ser Tyr Leu Leu Pro Xaa Thr Asp Met Tyr
            165             170             175

Asp Asn Gly Ser Leu Asn Ser Leu Phe Glu Ser Ile His Gly Val Pro
            180             185             190

Pro Thr Gln Arg Trp Gln Pro Asp Ser Thr Phe Lys Asp Asp Pro Gln
    195             200             205

Glu Ser Met Leu Phe Pro Asp Ile Leu Lys Thr Ser Pro Glu Pro Pro
    210             215             220

Cys Pro Glu Asp Tyr Pro Ser Leu Lys Ser Asp Phe Glu Tyr Thr Leu
225             230             235             240

Gly Ser Pro Lys Ala Ile His Ile Lys Ser Gly Glu Ser Pro Met Ala
            245             250             255

Tyr Leu Asn Lys Gly Gln Phe Tyr Pro Val Thr Leu Arg Thr Pro Ala
            260             265             270

Gly Gly Lys Gly Leu Ala Leu Ser Ser Asn Lys Val Lys Ser Val Val
```

- 24 -

```
        275                    280                    285

Met Val Val Phe Asp Asn Glu Lys Val Pro Val Glu Gln Leu Arg Phe
    290             295             300

Trp Lys His Trp His Ser Arg Gln Pro Thr Ala Lys Gln Arg Val Ile
305             310             315             320

Asp Val Ala Asp Cys Lys Glu Asn Phe Asn Thr Val Glu His Ile Glu
            325             330             335

Glu Val Ala Tyr Asn Ala Leu Ser Phe Val Trp Asn Val Asn Glu Glu
            340             345             350

Ala Lys Val Phe Ile Gly Val Asn Cys Leu Ser Thr Asp Phe Ser Ser
        355             360             365

Gln Lys Gly Val Lys Gly Val Pro Leu Asn Leu Gln Ile Asp Thr Tyr
    370             375             380

Asp Cys Gly Leu Gly Thr Glu Arg Leu Val His Arg Ala Val Cys Gln
385             390             395             400

Ile Lys Ile Phe Cys Asp Lys Gly Ala Glu Arg Lys Met Arg Asp Asp
            405             410             415

Glu Arg Lys Gln Phe Arg Arg Lys Val Lys Cys Pro Asp Ser Ser Asn
            420             425             430

Ser Gly Val Lys Gly Cys Leu Leu Ser Gly Phe Arg Gly Asn Glu Thr
        435             440             445

Thr Tyr Leu Arg Pro Glu Thr Asp Leu Glu Thr Pro Pro Val Leu Phe
    450             455             460

Ile Pro Asn Val His Phe Ser Ser Leu Gln Arg Ser Gly Gly Ala Ala
465             470             475             480

Pro Ser Ala Gly Pro Ser Ser Ser Asn Arg Leu Pro Leu Lys Arg Thr
            485             490             495

Cys Ser Pro Phe Thr Glu Glu Phe Glu Pro Leu Pro Ser Lys Gln Ala
            500             505             510
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Lys Glu Gly Asp Leu Gln Arg Val Leu Leu Tyr Val Arg Arg Glu Thr
        515                 520                 525


Glu Glu Val Phe Asp Ala Leu Met Leu Lys Thr Pro Asp Leu Lys Gly
        530                 535                 540


Leu Arg Asn Ala Ile Ser Glu Lys Tyr Gly Phe Pro Glu Glu Asn Ile
545                 550                 555                 560


Tyr Lys Val Tyr Lys Lys Cys Lys Arg Gly Ile Leu Val Asn Met Asp
                565                 570                 575


Asn Asn Ile Ile Gln His Tyr Ser Asn His Val Ala Phe Leu Leu Asp
                580                 585                 590


Met Gly Glu Leu Asp Gly Lys Ile Gln Ile Ile Leu Lys Glu Leu
        595                 600                 605
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caagtgctga aaaacgtgcc cttcaacatc gtcctccccc atagcaacca gctgggcatt     180

gataagagag gccatctgac agctcccgat acaacagtca ctgtctccat agcgaccatg     240

cctacccact ccatcaagac agaaatccag ccgcacggct tgctgtggg aatccctcca     300

gccgtgtacc actctgagcc caccgaacgc gtggtggttt ttgaccggag cctcagcact     360

gatcagttca gctctggcac tcagcccccc aatgctcagc ggaggactcc agactccacc     420
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- 26 -

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cggatgccgg gcatgaattc agaggactat gtctttgaca atgtttctgg gaacaacttt      540

gagtataccc tggaagcctc caagtcactg cggcagaagc aaggggacag cactatgaca      600

tacctgaata aaggccagtt ctatcctgtc accttaaagg aaggaagcag caatgaaggg      660

attcaccacc ctatcagcaa agttcgaagt gtgatcatgg tggttttgc tgaagacaaa      720

agcagagaag accagctgag acactggaag tactggcact cccgtcagca cacggccaaa      780

cagaggtgca ttgacattgc tgactacaaa gaaagtttca acactatcag caacattgag      840

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atctctgtga actgcttgag cacagatttc tcttctcaga agggtgtgaa gggcttgcca      960

ctcaacattc aaatcgacac atacagctat aacaaccgca gcaacaagcc ggttcaccgg      1020

gcctactgcc agataaaggt cttctgcgac aagggagctg aaaggaaaat tcgggatgaa      1080

gaacgaaaac agagcaagag aaaagtgtct gacgttaaag tgcagctgct tccctcacac      1140

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ctcaccctga cagagattta aggggcaggg gtggggggc gctcggctcc caggcgtggg      1680

aattcagtga agtgttcca gctgagaagc ccaggcacct accctgcaga accttaaata      1740

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acctgctcca ctacctgtca aagtctgcct gtgtccataa gagtggtggg ctactggctg      1980

gcgagagagg ggaaggcagt agcttgtctt tgaggctttt gtgttctcgc ctgacctcag      2040

tctaactctg actgccttga ggagtgggcc cagccctcag caataaaggg ctaagccttc      2100
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- 27 -

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aagttagctc tgttaaagct gcgttgtata taagtgcaat atctttttga aggtctgcct      2280

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cagatagtga aggcgagcag gaagatctac cttgaaatcc ctcttagaga agaggttaag      2400

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tatgaggtgt gtgtgcaggt gtcagccaag ctgtgcccat gcagagactc agcngtgtca      2640

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agcatcagct accgtgtgtt tgaactggaa ggcattcatg aatttacata actgtggcag      2760

gggaatgttt tgtgcacact aaatatttta agaacaaaac gaaactttac aatgtaaytt      2820

tataatgaat cctgtaacag aaatacaatt gcgggtttct ttaggttcag ggaactagaa      2880

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Val Thr Glu Gln Pro Leu Ile Ser Ala Gly Glu Asn Arg Val Gln Val
            20                  25                  30


Leu Lys Asn Val Pro Phe Asn Ile Val Leu Pro His Ser Asn Gln Leu
        35                  40                  45


Gly Ile Asp Lys Arg Gly His Leu Thr Ala Pro Asp Thr Thr Val Thr
    50                  55                  60
```

- 28 -

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Val Ser Ile Ala Thr Met Pro Thr His Ser Ile Lys Thr Glu Ile Gln
65                70                75                80


Pro His Gly Phe Ala Val Gly Ile Pro Pro Ala Val Tyr His Ser Glu
                 85                90                95


Pro Thr Glu Arg Val Val Val Phe Asp Arg Ser Leu Ser Thr Asp Gln
             100                105                110


Phe Ser Ser Gly Thr Gln Pro Pro Asn Ala Gln Arg Arg Thr Pro Asp
             115                120                125


Ser Thr Phe Ser Glu Thr Phe Lys Glu Gly Val Gln Glu Val Phe Phe
    130                135                140


Pro Ser Glu Leu Ser Leu Arg Met Pro Gly Met Asn Ser Glu Asp Tyr
145                150                155                160


Val Phe Asp Asn Val Ser Gly Asn Asn Phe Glu Tyr Thr Leu Glu Ala
                 165                170                175


Ser Lys Ser Leu Arg Gln Lys Gln Gly Asp Ser Thr Met Thr Tyr Leu
             180                185                190


Asn Lys Gly Gln Phe Tyr Pro Val Thr Leu Lys Glu Gly Ser Ser Asn
             195                200                205


Glu Gly Ile His His Pro Ile Ser Lys Val Arg Ser Val Ile Met Val
    210                215                220


Val Phe Ala Glu Asp Lys Ser Arg Glu Asp Gln Leu Arg His Trp Lys
225                230                235                240


Tyr Trp His Ser Arg Gln His Thr Ala Lys Gln Arg Cys Ile Asp Ile
                 245                250                255


Ala Asp Tyr Lys Glu Ser Phe Asn Thr Ile Ser Asn Ile Glu Glu Ile
             260                265                270


Ala Tyr Asn Ala Ile Ser Phe Thr Trp Asp Ile Asn Asp Glu Ala Lys
    275                280                285
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- 29 -

Val Phe Ile Ser Val Asn Cys Leu Ser Thr Asp Phe Ser Ser Gln Lys
    290   295   300

Gly Val Lys Gly Leu Pro Leu Asn Ile Gln Ile Asp Thr Tyr Ser Tyr
305   310   315   320

Asn Asn Arg Ser Asn Lys Pro Val His Arg Ala Tyr Cys Gln Ile Lys
                325   330   335

Val Phe Cys Asp Lys Gly Ala Glu Arg Lys Ile Arg Asp Glu Glu Arg
            340   345   350

Lys Gln Ser Lys Arg Lys Val Ser Asp Val Lys Val Gln Leu Leu Pro
        355   360   365

Ser His Lys Arg Thr Asp Ile Thr Val Phe Lys Pro Phe Leu Asp Leu
    370   375   380

Asp Thr Gln Pro Val Leu Phe Ile Pro Asp Val His Phe Thr Asn Leu
385   390   395   400

Gln Arg Gly Ser His Val Leu Ser Leu Pro Ser Glu Glu Leu Glu Gly
                405   410   415

Glu Gly Ser Val Leu Lys Arg Gly Pro Phe Gly Thr Glu Asp Asp Phe
            420   425   430

Gly Val Pro Pro Pro Ala Lys Leu Thr Arg Thr Glu Pro Lys Arg
            435   440   445

Val Leu Leu Tyr Val Arg Lys Glu Ser Glu Glu Val Phe Asp Ala Leu
    450   455   460

Met Leu Lys Thr Pro Ser Leu Lys Gly Leu Met Glu Ala Ile Ser Asp
465   470   475   480

Lys Tyr Asp Val Pro His Asp Lys Ile Gly Lys Ile Phe Lys Lys Cys
                485   490   495

Lys Lys Gly Ile Leu Val Asn Met Asp Asp Asn Ile Val Lys His Tyr
            500   505   510

Ser Asn Glu Asp Thr Phe Gln Leu Gln Ile Glu Glu Ala Gly Gly Ser

- 30 -

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Tyr Lys Leu Thr Leu Thr Glu Ile
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tacccacagc ggcgctccta taccagtgag gatgaagcct ggaagtcgtt cctggaaaac     240

cctctcactg cggcaaccaa agcgatgatg agcatcaacg gagacgaaga cagcgcggct     300

gcgctgggcc tgctctatga ctactacaag gtccccagag agcgccggtc atcagccgta     360

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gctcccgata aacagtcac tgtctccata gcgaccatgc ctacccactc catcaagaca     600

gaaatccagc cgcacggctt tgctgtggga atccctccag ccgtgtacca ctctgagccc     660

accgaacgcg tggtggtttt tgaccggagc ctcagcactg atcagttcag ctctggcact     720

cagcccccca atgctcagcg gaggactcca gactccacct tctccgagac cttcaaggag     780

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gaggactatg tctttgacaa tgtttctggg aacaactttg agtataccct ggaagcctcc     900

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cgttgtatat aagtgcaata tcttttttgaa ggtctgcctg taaatgtgta catatatgtc    2640

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- 32 -

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aatacaattg cgggtttctt taggttcagg gaactagaat aggtcatttg tatgagtagg    3240

attgttagcg gtatacgtar gttaaaaagt actctaatga agtatgtgaa caaaatagct    3300

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            20                  25                  30


Trp Lys Ser Phe Leu Glu Asn Pro Leu Thr Ala Ala Thr Lys Ala Met
        35                  40                  45


Met Ser Ile Asn Gly Asp Glu Asp Ser Ala Ala Ala Leu Gly Leu Leu
    50                  55                  60


Tyr Asp Tyr Tyr Lys Val Pro Arg Glu Arg Arg Ser Ser Ala Val Lys
65                  70                  75                  80


Pro Glu Gly Glu His Pro Glu Pro Glu His Ser Lys Arg Asn Ser Ile
                85                  90                  95
```

- 33 -

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Pro Asn Val Thr Glu Gln Pro Leu Ile Ser Ala Gly Glu Asn Arg Val
        100                 105                 110

Gln Val Leu Lys Asn Val Pro Phe Asn Ile Val Leu Pro His Ser Asn
        115                 120                 125

Gln Leu Gly Ile Asp Lys Arg Gly His Leu Thr Ala Pro Asp Thr Thr
        130                 135                 140

Val Thr Val Ser Ile Ala Thr Met Pro Thr His Ser Ile Lys Thr Glu
145                 150                 155                 160

Ile Gln Pro His Gly Phe Ala Val Gly Ile Pro Pro Ala Val Tyr His
                165                 170                 175

Ser Glu Pro Thr Glu Arg Val Val Val Phe Asp Arg Ser Leu Ser Thr
                180                 185                 190

Asp Gln Phe Ser Ser Gly Thr Gln Pro Pro Asn Ala Gln Arg Arg Thr
        195                 200                 205

Pro Asp Ser Thr Phe Ser Glu Thr Phe Lys Glu Gly Val Gln Glu Val
        210                 215                 220

Phe Phe Pro Ser Glu Leu Ser Leu Arg Met Pro Gly Met Asn Ser Glu
225                 230                 235                 240

Asp Tyr Val Phe Asp Asn Val Ser Gly Asn Asn Phe Glu Tyr Thr Leu
                245                 250                 255

Glu Ala Ser Lys Ser Leu Arg Gln Lys Gln Gly Asp Ser Thr Met Thr
                260                 265                 270

Tyr Leu Asn Lys Gly Gln Phe Tyr Pro Val Thr Leu Lys Glu Gly Ser
        275                 280                 285

Ser Asn Glu Gly Ile His His Pro Ile Ser Lys Val Arg Ser Val Ile
        290                 295                 300

Met Val Val Phe Ala Glu Asp Lys Ser Arg Glu Asp Gln Leu Arg His
305                 310                 315                 320
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- 34 -

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Trp Lys Tyr Trp His Ser Arg Gln His Thr Ala Lys Gln Arg Cys Ile
            325             330                 335


Asp Ile Ala Asp Tyr Lys Glu Ser Phe Asn Thr Ile Ser Asn Ile Glu
            340             345                 350


Glu Ile Ala Tyr Asn Ala Ile Ser Phe Thr Trp Asp Ile Asn Asp Glu
            355             360                 365


Ala Lys Val Phe Ile Ser Val Asn Cys Leu Ser Thr Asp Phe Ser Ser
    370             375                 380


Gln Lys Gly Val Lys Gly Leu Pro Leu Asn Ile Gln Ile Asp Thr Tyr
385             390                 395                 400


Ser Tyr Asn Asn Arg Ser Asn Lys Pro Val His Arg Ala Tyr Cys Gln
                405             410                 415


Ile Lys Val Phe Cys Asp Lys Gly Ala Glu Arg Lys Ile Arg Asp Glu
            420             425                 430


Glu Arg Lys Gln Ser Lys Arg Lys Val Ser Asp Val Lys Val Gln Leu
        435             440                 445


Leu Pro Ser His Lys Arg Thr Asp Ile Thr Val Phe Lys Pro Phe Leu
    450             455                 460


Asp Leu Asp Thr Gln Pro Val Leu Phe Ile Pro Asp Val His Phe Thr
465             470                 475                 480


Asn Leu Gln Arg Gly Ser His Val Leu Ser Leu Pro Ser Glu Glu Leu
            485             490                 495


Glu Gly Glu Gly Ser Val Leu Lys Arg Gly Pro Phe Gly Thr Glu Asp
            500             505                 510


Asp Phe Gly Val Pro Pro Pro Ala Lys Leu Thr Arg Thr Glu Glu Pro
            515             520                 525


Lys Arg Val Leu Leu Tyr Val Arg Lys Glu Ser Glu Glu Val Phe Asp
    530             535                 540
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- 35 -

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Ala Leu Met Leu Lys Thr Pro Ser Leu Lys Gly Leu Met Glu Ala Ile
545                 550                 555                 560


Ser Asp Lys Tyr Asp Val Pro His Asp Lys Ile Gly Lys Ile Phe Lys
                565                 570                 575


Lys Cys Lys Lys Gly Ile Leu Val Asn Met Asp Asp Asn Ile Val Lys
                580                 585                 590


His Tyr Ser Asn Glu Asp Thr Phe Gln Leu Gln Ile Glu Glu Ala Gly
        595                 600                 605


Gly Ser Tyr Lys Leu Thr Leu Thr Glu Ile
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gccttagtgc ccatgcccag tgaccctccc ttcaacaccc gaagagccta cacaagtgag   180

gatgaggcct ggaagtcata tctggagaac ccctgactg cggccaccaa ggcgatgatg   240

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gttcctcgag acaagagact tctgtctgtg agcaaagcaa gtgacagcca agaagaccag   360

gataaaagaa actgccttgg caccagtgaa gcccagatca atttgagcgg aggcgagaac   420

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aattcgaagc gcgagcagta cagtgtatcc atcaccgaga gctctgccgt catccccgtg   540

tcaggcatca ccgtggtgaa agccgaggat ttcacaccgg tgttcatggc cccccggtg   600

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gacagcacct acagcgagag ctttaaggac ggcgcctcgg agaaatttcg gagtacttct   780

gttggtgctg acgagtatac atatgaccag acgggaagtg tacatttca gtacaccctg   840

gaagccacca aatctctccg tcagaaacag ggggagggcc ccatgaccta cctcaacaaa   900

ggacaattct atgccataac actcagtgag actggagaca caaatgctt ccgacacccc   960
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- 36 -

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atcagcaaag  tcaggagtgt  ggtgatggtg  gtctttagtg  aagacaaaaa  ccgagatgag   1020

cagctgaaat  actggaagta  ctggcactcc  cggcagcaca  ctgccaagca  gagggtcctt   1080

gacattgctg  attacaagga  gagcttcaac  accatcggga  acattgaaga  gatcgcatac   1140

aatgctgttt  ccttcacctg  ggatgtgaac  gaggaggcaa  agattttat   caccgtgaat   1200

tgcctgagta  cagatttctc  ctcccaaaag  ggtgtaaaag  gacttcccct  gatgattcag   1260

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aagatggccg  ccataccgtt  acagaagaag  agtgacatca  cgtacttcaa  aaccatgccc   1500

gacctgcact  cacagcctgt  gctcttcata  ccagatgttc  actttgcaaa  cctacagagg   1560

accggacagg  tttattacaa  cacagacgat  gagcgagaag  gcagcagcgt  ccttgttaag   1620

cggatgttca  ggcccatgga  agaggagttt  ggtccaacac  cgtctaagca  gatcaaagaa   1680

gaaaacgtaa  aacgagtgct  tttatatgtg  aggaaggaga  cgatgacgt   cttcgatgct   1740

ctgatgctga  aatcacccac  ggtgaagggt  ctgatggaag  cgctgtctga  gaagtatggg   1800

ctgccagtgg  agaaaatcac  aaagctttat  aagaagagca  aaaagggcat  cctggtcaac   1860

atggatgaca  acatcattga  gcactattca  aatgaggaca  ccttcatcct  caacatggag   1920

agcatggtgg  aaggcttcaa  gatcacgctg  atggagatct  gagccctggg  tgtcccctcg   1980

ataggagctt  ttggtatact  ccttcctggg  agagatggga  tctctgccgc  cccaggacct   2040

ggagacccac  ccatctcact  cacctctcaa  gactgttaca  agactgctgg  gaaggggggc   2100

agggcccaag  gcccagtaat  ggacttcctt  caactcttcc  acttgctccc  tatggagctg   2160

aagcctgagc  ccctcagcaa  atttcttctc  gtgcc                                2195
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<212>  PRT
<213>  murine

<400>  14

Met Ser Gln Glu Ser Asp Asn Asn Lys Arg Leu Val Ala Leu Val Pro
1               5                   10                  15


Met Pro Ser Asp Pro Pro Phe Asn Thr Arg Arg Ala Tyr Thr Ser Glu
            20                  25                  30
```

- 37 -

```
Asp Glu Ala Trp Lys Ser Tyr Leu Glu Asn Pro Leu Thr Ala Ala Thr
        35              40              45


Lys Ala Met Met Ser Ile Asn Gly Asp Glu Asp Ser Ala Ala Ala Leu
    50              55              60


Gly Leu Leu Tyr Asp Tyr Tyr Lys Val Pro Arg Asp Lys Arg Leu Leu
65              70              75              80


Ser Val Ser Lys Ala Ser Asp Ser Gln Glu Asp Gln Asp Lys Arg Asn
            85              90              95


Cys Leu Gly Thr Ser Glu Ala Gln Ile Asn Leu Ser Gly Gly Glu Asn
            100             105             110


Arg Val Gln Val Leu Lys Thr Val Pro Val Asn Leu Cys Leu Ser Gln
        115             120             125


Asp His Met Glu Asn Ser Lys Arg Glu Gln Tyr Ser Val Ser Ile Thr
    130             135             140


Glu Ser Ser Ala Val Ile Pro Val Ser Gly Ile Thr Val Val Lys Ala
145             150             155             160


Glu Asp Phe Thr Pro Val Phe Met Ala Pro Pro Val His Tyr Pro Arg
                165             170             175


Ala Asp Ser Glu Glu Gln Arg Val Val Ile Phe Glu Gln Thr Gln Tyr
            180             185             190


Asp Leu Pro Ser Ile Ala Ser His Ser Ser Tyr Leu Lys Asp Asp Gln
        195             200             205


Arg Ser Thr Pro Asp Ser Thr Tyr Ser Glu Ser Phe Lys Asp Gly Ala
    210             215             220


Ser Glu Lys Phe Arg Ser Thr Ser Val Gly Ala Asp Glu Tyr Thr Tyr
225             230             235             240


Asp Gln Thr Gly Ser Gly Thr Phe Gln Tyr Thr Leu Glu Ala Thr Lys
            245             250             255
```

- 38 -

```
Ser Leu Arg Gln Lys Gln Gly Glu Gly Pro Met Thr Tyr Leu Asn Lys
        260             265             270


Gly Gln Phe Tyr Ala Ile Thr Leu Ser Glu Thr Gly Asp Asn Lys Cys
        275             280             285


Phe Arg His Pro Ile Ser Lys Val Arg Ser Val Val Met Val Val Phe
        290             295             300


Ser Glu Asp Lys Asn Arg Asp Glu Gln Leu Lys Tyr Trp Lys Tyr Trp
305             310             315             320


His Ser Arg Gln His Thr Ala Lys Gln Arg Val Leu Asp Ile Ala Asp
                325             330             335


Tyr Lys Glu Ser Phe Asn Thr Ile Gly Asn Ile Glu Glu Ile Ala Tyr
            340             345             350


Asn Ala Val Ser Phe Thr Trp Asp Val Asn Glu Glu Ala Lys Ile Phe
            355             360             365


Ile Thr Val Asn Cys Leu Ser Thr Asp Phe Ser Ser Gln Lys Gly Val
        370             375             380


Lys Gly Leu Pro Leu Met Ile Gln Ile Asp Thr Tyr Ser Tyr Asn Asn
385             390             395             400


Arg Ser Asn Lys Pro Ile His Arg Ala Tyr Cys Gln Ile Lys Val Phe
                405             410             415


Cys Asp Lys Gly Ala Glu Arg Lys Ile Arg Asp Glu Glu Arg Lys Gln
            420             425             430


Asn Arg Lys Lys Gly Lys Gly Gln Ala Ser Gln Ala Gln Cys Asn Asn
        435             440             445


Ser Ser Asp Gly Lys Met Ala Ala Ile Pro Leu Gln Lys Lys Ser Asp
        450             455             460


Ile Thr Tyr Phe Lys Thr Met Pro Asp Leu His Ser Gln Pro Val Leu
465             470             475             480
```

- 39 -

Phe Ile Pro Asp Val His Phe Ala Asn Leu Gln Arg Thr Gly Gln Val
            485   490   495

Tyr Tyr Asn Thr Asp Asp Glu Arg Glu Gly Ser Ser Val Leu Val Lys
            500   505   510

Arg Met Phe Arg Pro Met Glu Glu Glu Phe Gly Pro Thr Pro Ser Lys
        515   520   525

Gln Ile Lys Glu Glu Asn Val Lys Arg Val Leu Leu Tyr Val Arg Lys
    530   535   540

Glu Asn Asp Asp Val Phe Asp Ala Leu Met Leu Lys Ser Pro Thr Val
545   550   555   560

Lys Gly Leu Met Glu Ala Leu Ser Glu Lys Tyr Gly Leu Pro Val Glu
            565   570   575

Lys Ile Thr Lys Leu Tyr Lys Lys Ser Lys Lys Gly Ile Leu Val Asn
            580   585   590

Met Asp Asp Asn Ile Ile Glu His Tyr Ser Asn Glu Asp Thr Phe Ile
        595   600   605

Leu Asn Met Glu Ser Met Val Glu Gly Phe Lys Ile Thr Leu Met Glu
    610   615   620

Ile
625

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<211> 2831
<212> DNA
<213> murine

<220>
<221> CDS
<222> (200)..(2008)
<223>

<220>
<221> misc_feature
<222> (2806)..(2806)
<223> n = any nucleotide

- 40 -

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acatccagag cgcaacgtag agcaaacgct tccccgggca ggaagggaat gtctgtgtca     120

gaggagaatt aagagacgag tggtcagcag cgcctgcgag ccaaccagag acggatcgct     180

ggaacctcgg agaaggaag atg tcg aat gaa ctt gat ttc agg tct gtg cgg     232
                     Met Ser Asn Glu Leu Asp Phe Arg Ser Val Arg
                      1               5                      10

ttg ctg aag aat gac cct gtg agc ttc cag aag ttt ccc tac agt aat     280
Leu Leu Lys Asn Asp Pro Val Ser Phe Gln Lys Phe Pro Tyr Ser Asn
             15                  20                      25

gag gac gag gcc tgg aag aca tac ctg gag aac cct ttg acg gct gcc     328
Glu Asp Glu Ala Trp Lys Thr Tyr Leu Glu Asn Pro Leu Thr Ala Ala
         30                  35                      40

acc aaa gcc atg atg aga gtc aac ggg gac gag gag agt gtg gct gct     376
Thr Lys Ala Met Met Arg Val Asn Gly Asp Glu Glu Ser Val Ala Ala
     45                  50                      55

ctg agc ttc ctc tac gac tac tat atg ggt ccc aag gag aag cgg ata     424
Leu Ser Phe Leu Tyr Asp Tyr Tyr Met Gly Pro Lys Glu Lys Arg Ile
60                  65                  70                      75

ctg tcc tcc agc act ggt ggc cgg aat gac caa gga aag aag ttc tac     472
Leu Ser Ser Ser Thr Gly Gly Arg Asn Asp Gln Gly Lys Lys Phe Tyr
                 80                  85                      90

cac agc atg gac tat gag ccg gat ctt gcc ccc ctc gag agc ccc aca     520
His Ser Met Asp Tyr Glu Pro Asp Leu Ala Pro Leu Glu Ser Pro Thr
                 95                 100                     105

cac ctc atg aaa ttt ttg aca gag aac gtg tct gga agt cca gac tac     568
His Leu Met Lys Phe Leu Thr Glu Asn Val Ser Gly Ser Pro Asp Tyr
             110                 115                     120

aca gac cag ctc aag aaa aac aat ctg cta ggc ttg gag ggg gtt cta     616
Thr Asp Gln Leu Lys Lys Asn Asn Leu Leu Gly Leu Glu Gly Val Leu
         125                 130                     135

ccc acc ccc ggc aag acc aat acc gtc ccc cca ggt ccg agt aaa ctg     664
Pro Thr Pro Gly Lys Thr Asn Thr Val Pro Pro Gly Pro Ser Lys Leu
140                 145                 150                     155

gaa gcc agc tcc atg gac agc tac ctc ttg ccc gcc agt gac ata tat     712
Glu Ala Ser Ser Met Asp Ser Tyr Leu Leu Pro Ala Ser Asp Ile Tyr
                 160                 165                     170

gac aat ggc tcc ctc aac tca tta ttt gag agc att cat ggg gtt cca     760
Asp Asn Gly Ser Leu Asn Ser Leu Phe Glu Ser Ile His Gly Val Pro
             175                 180                     185

ccc aca cag cgc tgg cag cca gac agc acc ttc aaa gat gac cca cag     808
Pro Thr Gln Arg Trp Gln Pro Asp Ser Thr Phe Lys Asp Asp Pro Gln
```

- 41 -

```
           190                   195                   200
gag tct ctg ctc ttc cct gat att ctg aag aca tcc ccg gac ccc cca      856
Glu Ser Leu Leu Phe Pro Asp Ile Leu Lys Thr Ser Pro Asp Pro Pro
    205                   210                   215

tgc cca gag gat tat cca ggc ctc aag agt gac ttt gaa tac acc ctg      904
Cys Pro Glu Asp Tyr Pro Gly Leu Lys Ser Asp Phe Glu Tyr Thr Leu
220                   225                   230                   235

ggc tcc ccc aaa gcc att cac atc aaa gca ggg gag tca ccc atg gcc      952
Gly Ser Pro Lys Ala Ile His Ile Lys Ala Gly Glu Ser Pro Met Ala
                240                   245                   250

tac ctc aac aag ggt cag ttc tac ccc gtc acc cta cgc acc cca gca     1000
Tyr Leu Asn Lys Gly Gln Phe Tyr Pro Val Thr Leu Arg Thr Pro Ala
                255                   260                   265

gga ggg aaa ggc ctc gct ctg tcc tcc agc aaa gtc aag agc gtg gtg     1048
Gly Gly Lys Gly Leu Ala Leu Ser Ser Ser Lys Val Lys Ser Val Val
                270                   275                   280

atg gtc gtg ttc gat aat gac aag gtc ccc gtg gag cag ctg cgt ttc     1096
Met Val Val Phe Asp Asn Asp Lys Val Pro Val Glu Gln Leu Arg Phe
    285                   290                   295

tgg agg cac tgg cat tcc cgg cag ccc acc gcc aag cag cgc gtc atc     1144
Trp Arg His Trp His Ser Arg Gln Pro Thr Ala Lys Gln Arg Val Ile
300                   305                   310                   315

gac gta gct gac tgt aag gaa aac ttc aac acg gtc cag cac att gaa     1192
Asp Val Ala Asp Cys Lys Glu Asn Phe Asn Thr Val Gln His Ile Glu
                320                   325                   330

gag gtg gcc tat aac gcg ctg tcc ttt gtg tgg aat gtc aac gag gaa     1240
Glu Val Ala Tyr Asn Ala Leu Ser Phe Val Trp Asn Val Asn Glu Glu
                335                   340                   345

gcc aag gtg ttt atc ggt gtc aac tgt ctg agc aca gac ttc tcc tcg     1288
Ala Lys Val Phe Ile Gly Val Asn Cys Leu Ser Thr Asp Phe Ser Ser
                350                   355                   360

cag aag gga gtg aag ggt gtc ccc ctg aac ttg caa att gac acc tat     1336
Gln Lys Gly Val Lys Gly Val Pro Leu Asn Leu Gln Ile Asp Thr Tyr
    365                   370                   375

gac tgt gga gca ggc act gag cgc ctg gta cac cgt gct gtc tgc cag     1384
Asp Cys Gly Ala Gly Thr Glu Arg Leu Val His Arg Ala Val Cys Gln
380                   385                   390                   395

atc aag atc ttc tgt gat aag gga gct gag agg aag atg cgc gat gat     1432
Ile Lys Ile Phe Cys Asp Lys Gly Ala Glu Arg Lys Met Arg Asp Asp
                400                   405                   410

gaa cgg aag cag ttt cga agg aag gtc aag tgc cca gac tcc agt aac     1480
Glu Arg Lys Gln Phe Arg Arg Lys Val Lys Cys Pro Asp Ser Ser Asn
    415                   420                   425
```

- 42 -

```
aat gca gga atc aag ggc tgc ctg ctg tca ggc ttc agg ggc aat gag      1528
Asn Ala Gly Ile Lys Gly Cys Leu Leu Ser Gly Phe Arg Gly Asn Glu
        430                 435                 440

acc aca tac ttg cgg cca gaa act gac ctg gag acc cag cct gtg ttg      1576
Thr Thr Tyr Leu Arg Pro Glu Thr Asp Leu Glu Thr Gln Pro Val Leu
    445                 450                 455

ttt atc ccc aat ctg cat ttt tcc agc cta cag cgc cca gga ggg gtt      1624
Phe Ile Pro Asn Leu His Phe Ser Ser Leu Gln Arg Pro Gly Gly Val
460                 465                 470                 475

gtc ccc tca gca gga cac agc agc tct gac agg ctg cct ctg aag cga      1672
Val Pro Ser Ala Gly His Ser Ser Ser Asp Arg Leu Pro Leu Lys Arg
                480                 485                 490

acc tgc tca ccc ttt gct gag gag ttt gag cct ctt cct tct aaa caa      1720
Thr Cys Ser Pro Phe Ala Glu Glu Phe Glu Pro Leu Pro Ser Lys Gln
            495                 500                 505

gcc aag gaa gat gac ctt cag aga gtt ctg ttg tat gtg agg agg gag      1768
Ala Lys Glu Asp Asp Leu Gln Arg Val Leu Leu Tyr Val Arg Arg Glu
        510                 515                 520

aca gag gag gtg ttt gac gcg ctc atg ttg aag acc ccg gac ctg aag      1816
Thr Glu Glu Val Phe Asp Ala Leu Met Leu Lys Thr Pro Asp Leu Lys
    525                 530                 535

ggc ctg agg aat gcg atc tct gag aag tac ggc ctc ccc gag gag aat      1864
Gly Leu Arg Asn Ala Ile Ser Glu Lys Tyr Gly Leu Pro Glu Glu Asn
540                 545                 550                 555

att tgc aaa gtc tac aag aaa tgc aag cga ggc atc ctg gtt aac atg      1912
Ile Cys Lys Val Tyr Lys Lys Cys Lys Arg Gly Ile Leu Val Asn Met
                560                 565                 570

gac aac aac atc atc caa cac tac agc aac cac gtg gcc ttc ctg ctg      1960
Asp Asn Asn Ile Ile Gln His Tyr Ser Asn His Val Ala Phe Leu Leu
            575                 580                 585

gac atg ggt gag ctg gac ggc aag atc cag atc atc ctg aag gag cta      2008
Asp Met Gly Glu Leu Asp Gly Lys Ile Gln Ile Ile Leu Lys Glu Leu
        590                 595                 600
```

tgagggcccg gcctcaagcg tcccacaccc ggggcccggc tcaagccacg tacaacctct   2068

tctgtgtcag ctgttacttg aaatgccttt ctttgggaaa gaggtctcgc aagcaaccaa   2128

ctcggtgatg tccaagccag ggagagacca agaaggttcc aggatctaaa tgtcccaccc   2188

aggctcgaac tcactccaga gcttcctgaa agcacccagc ccaccggaga gtctgagcaa   2248

cacagaccca actgcctgct ttctcttcta agtcccgctg cagaggccct tacaggggac   2308

gggggtcaca ccaccttctc tgcagggcta cacccgctgt ctcgatcggt tctgacgttc   2368

- 43 -

```
actgtttcct ttctaccaac ttcagaccag agagttctca cactttggcc aaataacttg     2428

aaaactcgtg actttcacag cagatgcctt tgtgaggccc ttggagagga aactttctta     2488

ttgacttcct cggcacaaga tgtaagtcac catcatcgag ctgacaggaa caaataccct     2548

tgccacctac tgttgtacac atttcttatt tacagttttc attatgtgat tatatatata     2608

tatatgtaag tatatattat gtacatatat gcaacatttt gtatgtccat gttacatttt     2668

tatcatttca aaaatatgta tttcatattt cttgaactat tttttagct gttattcgat      2728

tatgcatttt gtatatcata gggtttagta ataaaagcct acccatgcac acttaaaaaa     2788

aaaaaaaaaa aaatatcnag cttatcgata ccgtcgacct cga                       2831
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<213>    murine

<220>
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<222>    (2806)..(2806)
<223>    n = any nucleotide

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1               5                   10                  15


Pro Val Ser Phe Gln Lys Phe Pro Tyr Ser Asn Glu Asp Glu Ala Trp
                20                  25                  30


Lys Thr Tyr Leu Glu Asn Pro Leu Thr Ala Ala Thr Lys Ala Met Met
            35                  40                  45


Arg Val Asn Gly Asp Glu Glu Ser Val Ala Ala Leu Ser Phe Leu Tyr
        50                  55                  60


Asp Tyr Tyr Met Gly Pro Lys Glu Lys Arg Ile Leu Ser Ser Ser Thr
65                  70                  75                  80


Gly Gly Arg Asn Asp Gln Gly Lys Lys Phe Tyr His Ser Met Asp Tyr
                85                  90                  95


Glu Pro Asp Leu Ala Pro Leu Glu Ser Pro Thr His Leu Met Lys Phe
                100                 105                 110
```

- 44 -

Leu Thr Glu Asn Val Ser Gly Ser Pro Asp Tyr Thr Asp Gln Leu Lys
        115   120   125

Lys Asn Asn Leu Leu Gly Leu Glu Gly Val Leu Pro Thr Pro Gly Lys
        130   135   140

Thr Asn Thr Val Pro Pro Gly Pro Ser Lys Leu Glu Ala Ser Ser Met
145   150   155   160

Asp Ser Tyr Leu Leu Pro Ala Ser Asp Ile Tyr Asp Asn Gly Ser Leu
                165   170   175

Asn Ser Leu Phe Glu Ser Ile His Gly Val Pro Pro Thr Gln Arg Trp
                180   185   190

Gln Pro Asp Ser Thr Phe Lys Asp Asp Pro Gln Glu Ser Leu Leu Phe
        195   200   205

Pro Asp Ile Leu Lys Thr Ser Pro Asp Pro Pro Cys Pro Glu Asp Tyr
        210   215   220

Pro Gly Leu Lys Ser Asp Phe Glu Tyr Thr Leu Gly Ser Pro Lys Ala
225   230   235   240

Ile His Ile Lys Ala Gly Glu Ser Pro Met Ala Tyr Leu Asn Lys Gly
                245   250   255

Gln Phe Tyr Pro Val Thr Leu Arg Thr Pro Ala Gly Gly Lys Gly Leu
                260   265   270

Ala Leu Ser Ser Ser Lys Val Lys Ser Val Val Met Val Val Phe Asp
        275   280   285

Asn Asp Lys Val Pro Val Glu Gln Leu Arg Phe Trp Arg His Trp His
        290   295   300

Ser Arg Gln Pro Thr Ala Lys Gln Arg Val Ile Asp Val Ala Asp Cys
305   310   315   320

Lys Glu Asn Phe Asn Thr Val Gln His Ile Glu Glu Val Ala Tyr Asn
                325   330   335

Ala Leu Ser Phe Val Trp Asn Val Asn Glu Glu Ala Lys Val Phe Ile

```
              340                   345                        350


Gly Val Asn Cys Leu Ser Thr Asp Phe Ser Ser Gln Lys Gly Val Lys
         355                   360                   365


Gly Val Pro Leu Asn Leu Gln Ile Asp Thr Tyr Asp Cys Gly Ala Gly
       370                   375                   380


Thr Glu Arg Leu Val His Arg Ala Val Cys Gln Ile Lys Ile Phe Cys
 385                   390                   395                   400


Asp Lys Gly Ala Glu Arg Lys Met Arg Asp Asp Glu Arg Lys Gln Phe
             405                   410                   415


Arg Arg Lys Val Lys Cys Pro Asp Ser Ser Asn Asn Ala Gly Ile Lys
             420                   425                   430


Gly Cys Leu Leu Ser Gly Phe Arg Gly Asn Glu Thr Thr Tyr Leu Arg
         435                   440                   445


Pro Glu Thr Asp Leu Glu Thr Gln Pro Val Leu Phe Ile Pro Asn Leu
     450                   455                   460


His Phe Ser Ser Leu Gln Arg Pro Gly Gly Val Val Pro Ser Ala Gly
 465                   470                   475                   480


His Ser Ser Ser Asp Arg Leu Pro Leu Lys Arg Thr Cys Ser Pro Phe
             485                   490                   495


Ala Glu Glu Phe Glu Pro Leu Pro Ser Lys Gln Ala Lys Glu Asp Asp
           500                   505                   510


Leu Gln Arg Val Leu Leu Tyr Val Arg Arg Glu Thr Glu Glu Val Phe
         515                   520                   525


Asp Ala Leu Met Leu Lys Thr Pro Asp Leu Lys Gly Leu Arg Asn Ala
     530                   535                   540


Ile Ser Glu Lys Tyr Gly Leu Pro Glu Glu Asn Ile Cys Lys Val Tyr
 545                   550                   555                   560


Lys Lys Cys Lys Arg Gly Ile Leu Val Asn Met Asp Asn Asn Ile Ile
             565                   570                   575
```

- 46 -

```
Gln His Tyr Ser Asn His Val Ala Phe Leu Leu Asp Met Gly Glu Leu
            580                     585             590

Asp Gly Lys Ile Gln Ile Ile Leu Lys Glu Leu
            595             600
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<213>    drosphila

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gcagcaacat caaatgttag gccaaaatgc acaaaccgcc agcaacaaag cagcaccaa    180

gcgaacgaaa caacaacagc tccacatacc acaaagagtg gcacattaga agcggccaaa    240

agcagccagc cgagagcatt gtgtaagcca aaggcccaga gagccaggct aaaagccccc    300

agacgcacaa caacaacaac aacaactaaa acagcacaaa gagtggcgaa aggtgcaccc    360

accagcaaaa cagcaacaac ggagcaacca acaacagcag cagcagcagc agcagccaca    420

tttcagttac agctccagac tcccaggttg cagactccca aagcaaacag actccagtcc    480

acgatccagc tccagttcca ccgatccgat ccactgctcc agcgtgctcg agtgccatag    540

atcctcacca agtgccaaaa tccgcatcct gatcccaaga gctcaaggca ccccggccca    600

aaattgagct gagaacgaaa cgaaggaagt tccttagtgc catagaaagc agttaatgaa    660

acaacgacta agacgaagat cgaccatcca gaaccggagg gagctaattg cgaacgaaag    720

aaaccacaaa gtgccttcca tcaatccgtt gataagtgat atttattatg tttatacttg    780

ccagcagccg aggcagcaac agcaatagca acaaccatag gggatcacgg catcgatgat    840

cagtccacga ccaagtccta gtgcaatccg gaatccagtt caaattagtt caataagccg    900

tatctaccac gtataatgtc cacatccacc gccacaacga gcgttatcac gtccaacgag    960

ctctcgctgt ccggccacgc ccacggtcac ggtcacgccc accagttgca ccagcacacc    1020

cacagccgcc taggagttgg cgttggtgtt ggcatcctta gcgacgcatc cctatcgccc    1080

atccaacaag gcagtggcgg ccacagcggc ggaggtaaca caaacagttc accactggcg    1140

cccaacggag tgccacttct cacaacaatg caccgatcac cggactcacc gcagccagaa    1200

ttggccacca tgacgaacgt caacgtgctg gatctgcaca cggataactc caagctgtac    1260
```

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gacaaggagg ctgtatttat atacgaaacg cccaaggtgg tgatgccagc ggatggcggg    1320

ggtggcaata attccgatga aggtcatgcc atcgatgcgc ggattgcggc ccaaatgggc    1380

aaccaagccc agcaacagca gcagcagcaa cagcagacgg aacaccagcc gctggccaag    1440

atcgagttcg atgagaacca gataatccgg gtggtgggac caaatggcga gcaacagcaa    1500

atcatctcgc gggagatcat caatggggag catcatatcc tgtcgcgaaa cgaggctggt    1560

gagcacattc tcacacggat cgtcagtgat ccctccaagt tgatgcccaa tgacaatgca    1620

gtggccacgg ccatgtacaa ccaggcccaa aagatgaaca atgatcacgg gcaggcggta    1680

tatcagacat caccattgcc gctagacgcg tctgtattgc attatagtgg cggcaatgat    1740

tcgaatgtaa ttaagacgga ggccgatatc tacgaggatc acaagaaaca tgcggctgca    1800

gcagcagctg ctgccggcgg aggatccatc atatacacca catccgatcc gaacggagtg    1860

aatgtgaaac aactgcccca tttgacggta ccccaaaaac ttgatcccga cctctatcaa    1920

gccgataagc atatagattt gatctacaac gatggcagca agacggtgat ttactccact    1980

acggatcaga agagtttgga aatatactcg ggcggcgaca tcggcagcct ggtgtccgac    2040

ggccaagtgg tggtccaggc gggactgccg tatgccacca ccaccggagc cggcggccag    2100

cccgtctata tcgtggccga cggtgccttg ccagcgggag tcgaggagca tctgcagagt    2160

ggaaagctca atggccagac cacacctatc gatgtctctg cctatcgca aaatgagatt    2220

caaggctttt tgctcggctc acacccctcg tcatcggcga cggtaagcac aaccggcgtt    2280

gtctccacga caacgatctc gcatcaccag caacagcagc agcagcagca acagcaacag    2340

cagcagcagc agcagcaaca ccagcagcag cagcaacatc ccggcgacat tgttagtgcc    2400

gctggcgtgg ggagcacggg ctccattgtc tcctctgcgg cgcaacagca gcagcagcag    2460

caactaatta gcatcaaacg agagcccgaa gacttgcgca aggatcccaa gaatggcaac    2520

attgccggtg cagcaacagc aaatggaccc ggttcggtca taacccaaaa gtcctttgat    2580

tatacggaat tgtgccagcc gggcacgctg atcgatgcca atggcagcat acccgtcagc    2640

gtgaacagca tccagcagag aacggcggtc catggcagcc agaacagtcc caccacatcg    2700

ctggtggaca ccagcaccaa tggatccacg cgatcgcggc cctggcacga ctttggacgt    2760

cagaatgatg ccgacaaaat acaaatacca aaaatcttca caaacgtggg cttccgatat    2820

cacctggaga gccccatcag ttcatcgcag aggcgcgagg acgatcgcat cacctacatc    2880

aacaagggtc aattctatgg aataacgctg gagtatgtgc acgatgcgga aaagcccatt    2940
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- 48 -

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aagaacacca ccgtcaagag tgtgatcatg ctaatgttcc gcgaggagaa gagtcccgag   3000
gatgagatca aggcctggca attctggcac agtcgtcagc attccgtgaa gcagagaatc   3060
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ccatagagcc taagtctaaa tatcgtagtt ataataatgg gatccgcaac aaatcgagtt   4260
gcaacgaatg ttaagaacgc taacacaata cgcatgtaaa atgatacttt aaaattgatt   4320
tagttatttt agcaacaatg agattatcta aaattgtttg atcaaatttt acattctcgc   4380
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tatgacctta ggtccagggc aagtatgagt taccgaatct atctattagg tgcatctaac   4620
gaaaggaatc attagctctg cacgaactct agccgtagcc tattgtaatc catttgtatg   4680
```

- 49 -

```
tttggcttaa  gcgttttact  tgttgaatat  aaagtgtaaa  attattttg  aaaaaaaaaa      4740

acccacacaa  aacacaaatc  gtttgttcta  tatttctgtt  tcaaaactaa  ctcgttaccc      4800

acaatccccct  ctgttatgta  taattaggat  ctctgtacac                             4840
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<212>    PRT
<213>    murine

<400>    18
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Met Ser Thr Ser Thr Ala Thr Thr Ser Val Ile Thr Ser Asn Glu Leu
1               5                   10                  15


Ser Leu Ser Gly His Ala His Gly His Gly His Ala His Gln Leu His
            20                  25                  30


Gln His Thr His Ser Arg Leu Gly Val Gly Val Gly Val Gly Ile Leu
        35                  40                  45


Ser Asp Ala Ser Leu Ser Pro Ile Gln Gln Gly Ser Gly Gly His Ser
    50                  55                  60


Gly Gly Gly Asn Thr Asn Ser Ser Pro Leu Ala Pro Asn Gly Val Pro
65                  70                  75                  80


Leu Leu Thr Thr Met His Arg Ser Pro Asp Ser Pro Gln Pro Glu Leu
                85                  90                  95


Ala Thr Met Thr Asn Val Asn Val Leu Asp Leu His Thr Asp Asn Ser
                100                 105                 110


Lys Leu Tyr Asp Lys Glu Ala Val Phe Ile Tyr Glu Thr Pro Lys Val
        115                 120                 125


Val Met Pro Ala Asp Gly Gly Gly Asn Asn Ser Asp Glu Gly His
        130                 135                 140


Ala Ile Asp Ala Arg Ile Ala Ala Gln Met Gly Asn Gln Ala Gln Gln
145                 150                 155                 160


Gln Gln Gln Gln Gln Gln Gln Thr Glu His Gln Pro Leu Ala Lys Ile
                165                 170                 175
```

- 50 -

```
Glu Phe Asp Glu Asn Gln Ile Ile Arg Val Val Gly Pro Asn Gly Glu
        180                 185                 190

Gln Gln Gln Ile Ile Ser Arg Glu Ile Ile Asn Gly Glu His His Ile
        195                 200                 205

Leu Ser Arg Asn Glu Ala Gly Glu His Ile Leu Thr Arg Ile Val Ser
    210                 215                 220

Asp Pro Ser Lys Leu Met Pro Asn Asp Asn Ala Val Ala Thr Ala Met
225                 230                 235                 240

Tyr Asn Gln Ala Gln Lys Met Asn Asn Asp His Gly Gln Ala Val Tyr
                245                 250                 255

Gln Thr Ser Pro Leu Pro Leu Asp Ala Ser Val Leu His Tyr Ser Gly
            260                 265                 270

Gly Asn Asp Ser Asn Val Ile Lys Thr Glu Ala Asp Ile Tyr Glu Asp
        275                 280                 285

His Lys Lys His Ala Ala Ala Ala Ala Ala Ala Gly Gly Gly Ser
        290                 295                 300

Ile Ile Tyr Thr Thr Ser Asp Pro Asn Gly Val Asn Val Lys Gln Leu
305                 310                 315                 320

Pro His Leu Thr Val Pro Gln Lys Leu Asp Pro Asp Leu Tyr Gln Ala
                325                 330                 335

Asp Lys His Ile Asp Leu Ile Tyr Asn Asp Gly Ser Lys Thr Val Ile
            340                 345                 350

Tyr Ser Thr Thr Asp Gln Lys Ser Leu Glu Ile Tyr Ser Gly Gly Asp
        355                 360                 365

Ile Gly Ser Leu Val Ser Asp Gly Gln Val Val Val Gln Ala Gly Leu
    370                 375                 380

Pro Tyr Ala Thr Thr Thr Gly Ala Gly Gly Gln Pro Val Tyr Ile Val
385                 390                 395                 400
```

Ala Asp Gly Ala Leu Pro Ala Gly Val Glu Glu His Leu Gln Ser Gly
            405   410   415

Lys Leu Asn Gly Gln Thr Thr Pro Ile Asp Val Ser Gly Leu Ser Gln
            420   425   430

Asn Glu Ile Gln Gly Phe Leu Leu Gly Ser His Pro Ser Ser Ser Ala
            435   440   445

Thr Val Ser Thr Thr Gly Val Val Ser Thr Thr Thr Ile Ser His His
        450   455   460

Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln
465   470   475   480

Gln His Gln Gln Gln Gln Gln His Pro Gly Asp Ile Val Ser Ala Ala
            485   490   495

Gly Val Gly Ser Thr Gly Ser Ile Val Ser Ser Ala Ala Gln Gln Gln
            500   505   510

Gln Gln Gln Gln Leu Ile Ser Ile Lys Arg Glu Pro Glu Asp Leu Arg
            515   520   525

Lys Asp Pro Lys Asn Gly Asn Ile Ala Gly Ala Ala Thr Ala Asn Gly
        530   535   540

Pro Gly Ser Val Ile Thr Gln Lys Ser Phe Asp Tyr Thr Glu Leu Cys
545   550   555   560

Gln Pro Gly Thr Leu Ile Asp Ala Asn Gly Ser Ile Pro Val Ser Val
            565   570   575

Asn Ser Ile Gln Gln Arg Thr Ala Val His Gly Ser Gln Asn Ser Pro
            580   585   590

Thr Thr Ser Leu Val Asp Thr Ser Thr Asn Gly Ser Thr Arg Ser Arg
            595   600   605

Pro Trp His Asp Phe Gly Arg Gln Asn Asp Ala Asp Lys Ile Gln Ile
    610   615   620

- 52 -

Pro Lys Ile Phe Thr Asn Val Gly Phe Arg Tyr His Leu Glu Ser Pro
625   630   635   640

Ile Ser Ser Ser Gln Arg Arg Glu Asp Asp Arg Ile Thr Tyr Ile Asn
                    645   650   655

Lys Gly Gln Phe Tyr Gly Ile Thr Leu Glu Tyr Val His Asp Ala Glu
                660   665   670

Lys Pro Ile Lys Asn Thr Thr Val Lys Ser Val Ile Met Leu Met Phe
                675   680   685

Arg Glu Glu Lys Ser Pro Glu Asp Glu Ile Lys Ala Trp Gln Phe Trp
        690   695   700

His Ser Arg Gln His Ser Val Lys Gln Arg Ile Leu Asp Ala Asp Thr
705   710   715   720

Lys Asn Ser Val Gly Leu Val Gly Cys Ile Glu Glu Val Ser His Asn
                725   730   735

Ala Ile Ala Val Tyr Trp Asn Pro Leu Glu Ser Ser Ala Lys Ile Asn
                740   745   750

Ile Ala Val Gln Cys Leu Ser Thr Asp Phe Ser Ser Gln Lys Gly Gly
                755   760   765

Leu Pro Leu His Val Gln Ile Asp Thr Phe Glu Asp Pro Arg Asp Thr
        770   775   780

Ala Val Phe His Arg Gly Tyr Cys Gln Ile Lys Val Phe Cys Asp Lys
785   790   795   800

Gly Ala Glu Arg Lys Thr Arg Asp Glu Glu Arg Arg Ala Ala Lys Arg
                805   810   815

Lys Met Thr Ala Thr Gly Arg Lys Lys Leu Asp Glu Leu Tyr His Pro
                820   825   830

Val Thr Asp Arg Ser Glu Phe Tyr Gly Met Gln Asp Phe Ala Lys Pro
        835   840   845

Pro Val Leu Phe Ser Pro Ala Glu Asp Met Glu Lys Val Gly Gln Leu

```
           850                     855                     860


Gly Ile Gly Ala Ala Thr Gly Met Thr Phe Asn Pro Leu Ser Asn Gly
865                 870                 875                 880


Asn Ser Asn Ser Asn Ser His Ser Ser Leu Gln Ser Phe Tyr Gly His
                885                 890                 895


Glu Thr Asp Ser Pro Asp Leu Lys Gly Ala Ser Pro Phe Leu Leu His
                900                 905                 910


Gly Gln Lys Val Ala Thr Pro Thr Leu Lys Phe His Asn His Phe Pro
            915                 920                 925


Pro Asp Met Gln Thr Asp Lys Lys Asp His Ile Leu Asp Gln Asn Met
        930                 935                 940


Leu Thr Ser Thr Pro Leu Thr Asp Phe Gly Pro Pro Met Lys Arg Gly
945                 950                 955                 960


Arg Met Thr Pro Pro Thr Ser Glu Arg Val Met Leu Tyr Val Arg Gln
                965                 970                 975


Glu Asn Glu Glu Val Tyr Thr Pro Leu His Val Val Pro Pro Thr Thr
            980                 985                 990


Ile Gly Leu Leu Asn Ala Ile Glu Asn Lys Tyr Lys Ile Ser Thr Thr
            995                 1000                1005


Ser Ile Asn Asn Ile Tyr Arg Thr Asn Lys Lys Gly Ile Thr Ala
    1010                1015                1020


Lys Ile Asp Asp Asp Met Ile Ser Phe Tyr Cys Asn Glu Asp Ile
    1025                1030                1035


Phe Leu Leu Glu Val Gln Gln Ile Glu Asp Asp Leu Tyr Asp Val
    1040                1045                1050


Thr Leu Thr Glu Leu Pro Asn Gln
    1055                1060
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<213>    human

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<213>    human

<220>
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<223>    human p49 mgr


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aacccattcc ctcgacatag a                                           21


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<213>    human

<400>    21
agcgcgatga cacaggagta                                             20


<210>    22
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<213>    human

<400>    22
cgttgctatg gagacagtga                                             20


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ccgtttaaca aggacactgc                                             20


<210>    24
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ctggaagcca ccaaatctct                                             20
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<210>    26
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<400>    26
agtgccagag ctgaactgat                                                          20


<210>    27
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<400>    27
tccatgggtt ccttgagttc                                                          20


<210>    28
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<400>    28
agtgccagag ctgaactgat                                                          20


<210>    29
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<400>    29
aaaggggagc gagttcattg                                                          20


<210>    30
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<213>    murine

<400>    30
agagctctcg gtgatggata                                                          20


<210>    31
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- 56 -

<210> 213   drosophila dopa decarboxylase promoter

<400> 31
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<210> 32
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<212> DNA
<213> drosophila PCNA promoter

<400> 32
gggtaaaaag tgtgaacaat caaaccagtt ggca   34

<210> 33
<211> 84
<212> DNA
<213> human

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cccatccttc aataacagca acca   84

<210> 34
<211> 4747
<212> DNA
<213> Drosophila

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cgaaccgacc cgcccctca actttgcgc cctccagtag caatagcagc aatatgagca   120

gcagcaacat caaatgttag gccaaaatgc acaaccgcc agcaacaaag gcagcaccaa   180

gcgaacgaaa caacaacagc tccacatacc acaaagagtg gcacattaga agcggccaaa   240

agcagccagc cgagagcatt gtgtaagcca aaggcccaga gagccaggct aaaagccccc   300

agacgcacaa caacaacaac aacaactaaa acagcacaaa gagtggcgaa aggtgcaccc   360

accagcaaaa cagcaacaac ggagcaacca acaacagcag cagcagcagc agcagccaca   420

tttcagttac agctccagac tcccaggttg cagactccca aagcaaacag actccagtcc   480

acgatccagc tccagttcca ccgatccgat ccactgctcc agcgtgctcg agtgccatag   540

atcctcacca agtgccaaaa tccgcatcct gatcccaaga gctcaaggca ccccggccca   600

aaattgagct gagaacgaaa cgaaggaagt tccttagtgc catagaaagc agttaatgaa   660

acaacgacta agacgaagat cgaccatcca gaaccggagg gagctaattg cgaacgaaag   720

aaaccacaaa gtgccttcca tcaatccgtt gataagtgat atttattatg tttatacttg   780

- 57 -

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ccagcagccg aggcagcaac agcaatagca acaaccatag gggatcacgg catcgatgat    840

cagtccacga ccaagtccta gtgcaatccg gaatccagtt caaattagtt caataagccg    900

tatctaccac gtataatgtc cacatccacc gccacaacga gcgttatcac gtccaacgag    960

ctctcgctgt ccggccacgc ccacggtcac ggtcacgccc accagttgca ccagcacacc   1020

cacagccgcc taggagttgg cgttggtgtt ggcatcctta gcgacgcatc cctatcgccc   1080

atccaacaag gcagtggcgg ccacagcggc ggaggtaaca caaacagttc accactggcg   1140

cccaacggag tgccacttct cacaacaatg caccgatcac cggactcacc gcagccagaa   1200

ttggccacca tgacgaacgt caacgtgctg gatctgcaca cggataactc caagctgtac   1260

gacaaggagg ctgtatttat atacgaaacg cccaaggtgg tgatgccagc ggatggcggg   1320

ggtggcaata attccgatga aggtcatgcc atcgatgcgc ggattgcggc ccaaatgggc   1380

aaccaagccc agcaacagca gcagcagcaa cagcagacgg aacaccagcc gctggccaag   1440

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gagcacattc tcacacggat cgtcagtgat ccctccaagt tgatgcccaa tgacaatgca   1620

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tatcagacat caccattgcc gctagacgcg tctgtattgc attatagtgg cggcaatgat   1740

tcgaatgtaa ttaagacgga ggccgatatc tacgaggatc acaagaaaca tgcggctgca   1800

gcagcagctg ctgccggcgg aggatccatc atatacacca catccgatcc gaacggagtg   1860

aatgtgaaac aactgcccca tttgacggta ccccaaaaac ttgatcccga cctctatcaa   1920

gccgataagc atatagattt gatctacaac gatggcagca agacggtgat ttactccact   1980

acggatcaga agagtttgga aatatactcg ggcggcgaca tcggcagcct ggtgtccgac   2040

ggccaagtgg tggtccaggc gggactgccg tatgccacca ccaccggagc cggcggccag   2100

cccgtctata tcgtggccga cggtgccttg ccagcgggag tcgaggagca tctgcagagt   2160

ggaaagctca atggccagac cacacctatc gatgtctctg cctatcgca aaatgagatt   2220

caaggctttt tgctcggctc acacccctcg tcatcggcga cggtaagcac aaccggcgtt   2280

gtctccacga caacgatctc gcatcaccag caacagcagc agcagcagca acagcaacag   2340

cagcagcagc agcagcaaca ccagcagcag cagcaacatc ccggcgacat tgttagtgcc   2400

gctggcgtgg ggagcacggg ctccattgtc tcctctgcgg cgcaacagca gcagcagcag   2460
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- 58 -

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caactaatta gcatcaaacg agagcccgaa gacttgcgca aggatcccaa gaatggcaac   2520

attgccggtg cagcaacagc aaatggaccc ggttcggtca taacccaaaa gtcctttgat   2580

tatacggaat tgtgccagcc gggcacgctg atcgatgcca atggcagcat acccgtcagc   2640

gtgaacagca tccagcagag aacggcggtc catggcagcc agaacagtcc caccacatcg   2700

ctggtggaca ccagcaccaa tggatccacg cgatcgcggc cctggcacga ctttggacgt   2760

cagaatgatg ccgacaaaat acaaatacca aaaatcttca caaacgtggg cttccgatat   2820

cacctggaga gccccatcag ttcatcgcag aggcgcgagg acgatcgcat cacctacatc   2880

aacaagggtc aattctatgg aataacgctg gagtatgtgc acgatgcgga aaagcccatt   2940

aagaacacca ccgtcaagag tgtgatcatg ctaatgttcc gcgaggagaa gagtcccgag   3000

gatgagatca aggcctggca attctggcac agtcgtcagc attccgtgaa gcagagaatc   3060

ttggatgcag atacgaagaa ctcggttggc ctcgttggct gcatcgagga agtgtcgcac   3120

aatgccatcg ccgtctactg gaatccgctg gagagctccg ccaagatcaa cattgcggtt   3180

cagtgcttga gcacggattt cagcagtcaa aagggaggcc tgccgctgca cgtacaaatc   3240

gacacatttg aggaccccag agatacggcg gtcttccacc gcggctactg tcagataaag   3300

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tcaccgttcc tgctccacgg ccagaaggtg gccacgccga cgctcaagtt ccacaaccat   3600

tttccgcccg acatgcagac cgataagaag gatcacatac tggaccagaa catgttgacc   3660

agcacacccc tgaccgactt tggtccgccg atgaagcgcg gcaggatgac gccgccgacc   3720

tcggaacgcg tgatgctgta cgtgcggcag gagaacgagg aggtgtatac accgttgcac   3780

gtggtgccgc ccaccacgat cggcctgcta aatgcgattg aaaacaaata caaaatctca   3840

acaacgagca taaataacat ttatcgcaca aacaagaagg ggattactgc gaaaattgac   3900

gatgacatga tatcgttcta ctgcaacgag gacatctttc tgctggaggt gcaacagatc   3960

gaggacgacc tgtacgatgt gacgctcacg gagctgccca atcagtagcg ctggcagtac   4020

gggtagcacc cgctaaccgc actcaaaaaa aaaagcaaac aaacacacaa attacggaca   4080

caacaagttg tttcaataag ccattttcca tagagcctaa gtctaaatat cgtagttata   4140

ataatgggat ccgcaacaaa tcgagttgca acgaatgtta agaacgctaa cacaatacgc   4200
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- 59 -

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atgtaaaatg atactttaaa attgatttag ttattttagc aacaatgaga ttatctaaaa    4260

ttgtttgatc aaattttaca ttctcgctat gtctatagat aattctaagc ccgtaagccc    4320

ataagcgtaa tcgtaatcgt aatcgtaccg tgtatttatg ctcatatata aacaactata    4380

tatatatata tatatatata tatgtgcgga gtgcaacagt gtctgtccag taggagataa    4440

gtctcgtttc cgctcccctg cttatgctat gaccttaggt ccagggcaag tatgagttac    4500

cgaatctatc tattaggtgc atctaacgaa aggaatcatt agctctgcac gaactctagc    4560

cgtagcctat tgtaatccat ttgtatgttt ggcttaagcg ttttacttgt tgaatataaa    4620

gtgtaaaatt atttttgaaa aaaaaaaacc cacacaaaac acaaatcgtt tgttctatat    4680

ttctgtttca aaactaactc gttacccaca atcccctctg ttatgtataa ttaggatctc    4740

tgtacac                                                              4747
```

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<210>  35
<211>  1030
<212>  PRT
<213>  Drosophila

<400>  35
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```
Met Ser Thr Ser Thr Ala Thr Thr Ser Val Ile Thr Ser Asn Glu Leu
1               5                   10                  15


Ser Leu Ser Gly His Ala His Gly His Gly His Ala His Gln Leu His
            20                  25                  30


Gln His Thr His Ser Arg Leu Gly Val Gly Val Gly Val Gly Ile Leu
        35                  40                  45


Ser Asp Ala Ser Leu Ser Pro Ile Gln Gln Gly Ser Gly Gly His Ser
    50                  55                  60


Gly Gly Gly Asn Thr Asn Ser Ser Pro Leu Ala Pro Asn Gly Val Pro
65                  70                  75                  80


Leu Leu Thr Thr Met His Arg Ser Pro Asp Ser Pro Gln Pro Glu Leu
                85                  90                  95


Ala Thr Met Thr Asn Val Asn Val Leu Asp Leu His Thr Asp Asn Ser
                100                 105                 110
```

- 60 -

Lys Leu Tyr Asp Lys Glu Ala Val Phe Ile Tyr Glu Thr Pro Lys Val
        115   120   125

Val Met Pro Ala Asp Gly Gly Gly Gly Asn Asn Ser Asp Glu Gly His
    130   135   140

Ala Ile Asp Ala Arg Ile Ala Ala Gln Met Gly Asn Gln Ala Gln Gln
145   150   155   160

Gln Gln Gln Gln Gln Gln Gln Thr Glu His Gln Pro Leu Ala Lys Ile
            165   170   175

Glu Phe Asp Glu Asn Gln Ile Ile Arg Val Val Gly Pro Asn Gly Glu
            180   185   190

Gln Gln Gln Ile Ile Ser Arg Glu Ile Ile Asn Gly Glu His His Ile
        195   200   205

Leu Ser Arg Asn Glu Ala Gly Glu His Ile Leu Thr Arg Ile Val Ser
    210   215   220

Asp Pro Ser Lys Leu Met Pro Asn Asp Asn Ala Val Ala Thr Ala Met
225   230   235   240

Tyr Asn Gln Ala Gln Lys Met Asn Asn Asp His Gly Gln Ala Val Tyr
            245   250   255

Gln Thr Ser Pro Leu Pro Leu Asp Ala Ser Val Leu His Tyr Ser Gly
            260   265   270

Gly Asn Asp Ser Asn Val Ile Lys Thr Glu Ala Asp Ile Tyr Glu Asp
        275   280   285

His Lys Lys His Ala Ala Ala Ala Ala Ala Ala Gly Gly Gly Ser
    290   295   300

Ile Ile Tyr Thr Thr Ser Asp Pro Asn Gly Val Asn Val Lys Gln Leu
305   310   315   320

Pro His Leu Thr Val Pro Gln Lys Leu Asp Pro Asp Leu Tyr Gln Ala
            325   330   335

Asp Lys His Ile Asp Leu Ile Tyr Asn Asp Gly Ser Lys Thr Val Ile

- 61 -

```
              340                    345                    350

Tyr Ser Thr Thr Asp Gln Lys Ser Leu Glu Ile Tyr Ser Gly Gly Asp
        355                  360                  365

Ile Gly Ser Leu Val Ser Asp Gly Gln Val Val Val Gln Ala Gly Leu
        370                  375                  380

Pro Tyr Ala Thr Thr Thr Gly Ala Gly Gly Gln Pro Val Tyr Ile Val
385                  390                  395                  400

Ala Asp Gly Ala Leu Pro Ala Gly Val Glu Glu His Leu Gln Ser Gly
                405                  410                  415

Lys Leu Asn Gly Gln Thr Thr Pro Ile Asp Val Ser Gly Leu Ser Gln
                420                  425                  430

Asn Glu Ile Gln Gly Phe Leu Leu Gly Ser His Pro Ser Ser Ser Ala
        435                  440                  445

Thr Val Ser Thr Thr Gly Val Val Ser Thr Thr Thr Ile Ser His His
        450                  455                  460

Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln
465                  470                  475                  480

Gln His Gln Gln Gln Gln Gln His Pro Gly Asp Ile Val Ser Ala Ala
                485                  490                  495

Gly Val Gly Ser Thr Gly Ser Ile Val Ser Ser Ala Ala Gln Gln Gln
                500                  505                  510

Gln Gln Gln Gln Leu Ile Ser Ile Lys Arg Glu Pro Glu Asp Leu Arg
                515                  520                  525

Lys Asp Pro Lys Asn Gly Asn Ile Ala Gly Ala Ala Thr Ala Asn Gly
        530                  535                  540

Pro Gly Ser Val Ile Thr Gln Lys Ser Phe Asp Tyr Thr Glu Leu Cys
545                  550                  555                  560

Gln Pro Gly Thr Leu Ile Asp Ala Asn Gly Ser Ile Pro Val Ser Val
                565                  570                  575
```

Asn Ser Ile Gln Gln Arg Thr Ala Val His Gly Ser Gln Asn Ser Pro
                580   585   590

Thr Thr Ser Leu Val Asp Thr Ser Thr Asn Gly Ser Thr Arg Ser Arg
                595   600   605

Pro Trp His Asp Phe Gly Arg Gln Asn Asp Ala Asp Lys Ile Gln Ile
        610   615   620

Pro Lys Ile Phe Thr Asn Val Gly Phe Arg Tyr His Leu Glu Ser Pro
625   630   635   640

Ile Ser Ser Ser Gln Arg Arg Glu Asp Asp Arg Ile Thr Tyr Ile Asn
                645   650   655

Lys Gly Gln Phe Tyr Gly Ile Thr Leu Glu Tyr Val His Asp Ala Glu
                660   665   670

Lys Pro Ile Lys Asn Thr Thr Val Lys Ser Val Ile Met Leu Met Phe
        675   680   685

Arg Glu Glu Lys Ser Pro Glu Asp Glu Ile Lys Ala Trp Gln Phe Trp
        690   695   700

His Ser Arg Gln His Ser Val Lys Gln Arg Ile Leu Asp Ala Asp Thr
705   710   715   720

Lys Asn Ser Val Gly Leu Val Gly Cys Ile Glu Glu Val Ser His Asn
                725   730   735

Ala Ile Ala Val Tyr Trp Asn Pro Leu Glu Ser Ser Ala Lys Ile Asn
                740   745   750

Ile Ala Val Gln Cys Leu Ser Thr Asp Phe Ser Ser Gln Lys Gly Gly
                755   760   765

Leu Pro Leu His Val Gln Ile Asp Thr Phe Glu Asp Pro Arg Asp Thr
        770   775   780

Ala Val Phe His Arg Gly Tyr Cys Gln Ile Lys Val Phe Cys Asp Lys
785   790   795   800

- 63 -

Gly Ala Glu Arg Lys Thr Arg Asp Glu Glu Arg Arg Ala Ala Lys Arg
                805   810   815

Lys Met Thr Ala Thr Gly Arg Lys Lys Leu Asp Glu Leu Tyr His Pro
                820   825   830

Val Thr Asp Arg Ser Glu Phe Tyr Gly Met Gln Asp Phe Ala Lys Pro
                835   840   845

Pro Val Leu Phe Ser Pro Ala Glu Asp Met Glu Lys Ser Phe Tyr Gly
        850   855   860

His Glu Thr Asp Ser Pro Asp Leu Lys Gly Ala Ser Pro Phe Leu Leu
865   870   875   880

His Gly Gln Lys Val Ala Thr Pro Thr Leu Lys Phe His Asn His Phe
                885   890   895

Pro Pro Asp Met Gln Thr Asp Lys Lys Asp His Ile Leu Asp Gln Asn
                900   905   910

Met Leu Thr Ser Thr Pro Leu Thr Asp Phe Gly Pro Pro Met Lys Arg
                915   920   925

Gly Arg Met Thr Pro Pro Thr Ser Glu Arg Val Met Leu Tyr Val Arg
        930   935   940

Gln Glu Asn Glu Glu Val Tyr Thr Pro Leu His Val Val Pro Pro Thr
945   950   955   960

Thr Ile Gly Leu Leu Asn Ala Ile Glu Asn Lys Tyr Lys Ile Ser Thr
                965   970   975

Thr Ser Ile Asn Asn Ile Tyr Arg Thr Asn Lys Lys Gly Ile Thr Ala
                980   985   990

Lys Ile Asp Asp Asp Met Ile Ser Phe Tyr Cys Asn Glu Asp Ile Phe
        995   1000   1005

Leu Leu Glu Val Gln Gln Ile Glu Asp Asp Leu Tyr Asp Val Thr
        1010   1015   1020

- 64 -

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Leu Thr  Glu Leu Pro Asn Gln
    1025                1030
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<212>   DNA
<213>   Drosophila

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gcagcaacat caaatgttag gccaaaatgc acaaaccgcc agcaacaaag gcagcaccaa      180

gcgaacgaaa caacaacagc tccacatacc acaaagagtg gcacattaga agcggccaaa      240

agcagccagc cgagagcatt gtgtaagcca aaggcccaga gagccaggct aaaagccccc      300

agacgcacaa caacaacaac aacaactaaa acagcacaaa gagtggcgaa aggtgcaccc      360

accagcaaaa cagcaacaac ggagcaacca acaacagcag cagcagcagc agcagccaca      420

tttcagttac agctccagac tcccaggttg cagactccca aagcaaacag actccagtcc      480

acgatccagc tccagttcca ccgatccgat ccactgctcc agcgtgctcg agtgccatag      540

atcctcacca agtgccaaaa tccgcatcct gatcccaaga gctcaaggca ccccggccca      600

aaattgagct gagaacgaaa cgaaggaagt tccttagtgc catagaaagc agttaatgaa      660

acaacgacta agacgaagat cgaccatcca gaaccggagg gagctaattg cgaacgaaag      720

aaaccacaaa gtgccttcca tcaatccgtt gataagtgat atttattatg tttatacttg      780

ccagcagccg aggcagcaac agcaatagca caaccatag gggatcacgg catcgatgat      840

cagtccacga ccaagtccta gtgcaatccg gaatccagtt caaattagtt caataagccg      900

tatctaccac gtataatgtc cacatccacc gccacaacga gcgttatcac gtccaacgag      960

ctctcgctgt ccggccacgc ccacggtcac ggtcacgccc accagttgca ccagcacacc     1020

cacagccgcc taggagttgg cgttggtgtt ggcatcctta gcgacgcatc cctatcgccc     1080

atccaacaag gcagtggcgg ccacagcggc ggaggtaaca caaacagttc accactggcg     1140

cccaacggag tgccacttct cacaacaatg caccgatcac cggactcacc gcagccagaa     1200

ttggccacca tgacgaacgt caacgtgctg gatctgcaca cggataactc caagctgtac     1260

gacaaggagg ctgtatttat atacgaaacg cccaaggtgg tgatgccagc ggatggcggg     1320

ggtggcaata attccgatga aggtcatgcc atcgatgcgc ggattgcggc ccaaatgggc     1380

aaccagcccc agcaacagca gcagcagcaa cagcagacgg aacaccagcc gctggccaag     1440
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- 65 -

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atcgagttcg atgagaacca gataatccgg gtggtgggac caaatggcga gcaacagcaa   1500

atcatctcgc gggagatcat caatggggag catcatatcc tgtcgcgaaa cgaggctggt   1560

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tatcagacat caccattgcc gctagacgcg tctgtattgc attatagtgg cggcaatgat   1740

tcgaatgtaa ttaagacgga ggccgatatc tacgaggatc acaagaaaca tgcggctgca   1800

gcagcagctg ctgccggcgg aggatccatc atatacacca catccgatcc gaacggagtg   1860

aatgtgaaac aactgcccca tttgacggta ccccaaaaac ttgatcccga cctctatcaa   1920

gccgataagc atatagattt gatctacaac gatggcagca agacggtgat ttactccact   1980

acggatcaga agagtttgga aatatactcg ggcggcgaca tcggcagcct ggtgtccgac   2040

ggccaagtgg tggtccaggc gggactgccg tatgccacca ccaccggagc cggcggccag   2100

cccgtctata tcgtggccga cggtgccttg ccagcgggag tcgaggagca tctgcagagt   2160

ggaaagctca atggccagac cacacctatc gatgtctctg cctatcgca aaatgagatt    2220

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gtctccacga caacgatctc gcatcaccag caacagcagc agcagcagca acagcaacag   2340

cagcagcagc agcagcaaca ccagcagcag cagcaacatc ccggcgacat tgttagtgcc   2400

gctggcgtgg ggagcacggg ctccattgtc tcctctgcgg cgcaacagca gcagcagcag   2460

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attgccggtg cagcaacagc aaatggaccc ggttcggtca taacccaaaa gatcttgcac   2580

gtggatgcac caacggcaag tgaagctgat aggcccagca cacccagcag cagcatcaac   2640

agcactgaaa acactgaatc ggactcacag tcagtatcag gatcagaatc aggatcgccg   2700

ggagccagga ccacagccac actagagatg tatgcaacca cgggcggcac acagatctat   2760

ctacagacct cacatcccag cacggcgagc ggagcgggcg gcggcgccgg acccgctgga   2820

gccgccggcg gcggcggtgt gtccatgcag gcgcaaagtc ccagtccggg tccctatatc   2880

acggccaatg actatggcat gtacacggcc agtcgcctgc cacccggtcc cccgcccacc   2940

agcaccacca cgtttatagc ggagccctcc tactatcggg aatactttgc accggatggc   3000

caaggtggct atgtgccggc cagcacgagg tctttgtatg cgacgtggga cgtatccgta   3060

tctcagcccg cggagtggt cacctatgag ggccgctttg ccggcagcgt tcccccgccc   3120
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- 66 -

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gccaccacca ccgtgctaac cagcgtgcat caccaccagc aacagcagca gcaacaacag    3180

cagcatcaac agcagcagca gcagcaacag caccaccagc agcaacagca ccattcgcag    3240

gatggcaaga gcaatggcgg agcaacgcca ctctatgcca aagccattac ggcggcgggt    3300

ctaacggtgg atttgccaag tccggattcg ggcattggta cggatgccat tacaccgcgg    3360

gatcagacaa atatccaaca gtcctttgat tatacggaat tgtgccagcc gggcacgctg    3420

atcgatgcca atggcagcat acccgtcagc gtgaacagca tccagcagag aacggcggtc    3480

catggcagcc agaacagtcc caccacatcg ctggtggaca ccagcaccaa tggatccacg    3540

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cattttccgc ccgacatgca gaccgataag aaggatcaca tactggacca gaacatgttg    4560

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acctcggaac gcgtgatgct gtacgtgcgg caggagaacg aggaggtgta tacaccgttg    4680

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- 67 -

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ataataatgg  gatccgcaac  aaatcgagtt  gcaacgaatg  ttaagaacgc  taacacaata  5100

cgcatgtaaa  atgatacttt  aaaattgatt  tagttatttt  agcaacaatg  agattatcta  5160

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agccgtagcc  tattgtaatc  catttgtatg  tttggcttaa  gcgttttact  tgttgaatat  5520

aaagtgtaaa  attatttttg  aaaaaaaaaa  acccacacaa  aacacaaatc  gtttgttcta  5580

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<212>   PRT
<213>   Drosophila

<400>   37

Met Ser Thr Ser Thr Ala Thr Thr Ser Val Ile Thr Ser Asn Glu Leu
1               5                   10                  15


Ser Leu Ser Gly His Ala His Gly His Gly His Ala His Gln Leu His
                20                  25                  30


Gln His Thr His Ser Arg Leu Gly Val Gly Val Gly Val Gly Ile Leu
            35                  40                  45


Ser Asp Ala Ser Leu Ser Pro Ile Gln Gln Gly Ser Gly Gly His Ser
        50                  55                  60


Gly Gly Gly Asn Thr Asn Ser Ser Pro Leu Ala Pro Asn Gly Val Pro
65                  70                  75                  80
```

- 68 -

Leu Leu Thr Thr Met His Arg Ser Pro Asp Ser Pro Gln Pro Glu Leu
            85   90   95

Ala Thr Met Thr Asn Val Asn Val Leu Asp Leu His Thr Asp Asn Ser
            100   105   110

Lys Leu Tyr Asp Lys Glu Ala Val Phe Ile Tyr Glu Thr Pro Lys Val
            115   120   125

Val Met Pro Ala Asp Gly Gly Gly Gly Asn Asn Ser Asp Glu Gly His
    130   135   140

Ala Ile Asp Ala Arg Ile Ala Ala Gln Met Gly Asn Gln Ala Gln Gln
145   150   155   160

Gln Gln Gln Gln Gln Gln Gln Thr Glu His Gln Pro Leu Ala Lys Ile
            165   170   175

Glu Phe Asp Glu Asn Gln Ile Ile Arg Val Val Gly Pro Asn Gly Glu
            180   185   190

Gln Gln Gln Ile Ile Ser Arg Glu Ile Ile Asn Gly Glu His His Ile
            195   200   205

Leu Ser Arg Asn Glu Ala Gly Glu His Ile Leu Thr Arg Ile Val Ser
    210   215   220

Asp Pro Ser Lys Leu Met Pro Asn Asp Asn Ala Val Ala Thr Ala Met
225   230   235   240

Tyr Asn Gln Ala Gln Lys Met Asn Asn Asp His Gly Gln Ala Val Tyr
            245   250   255

Gln Thr Ser Pro Leu Pro Leu Asp Ala Ser Val Leu His Tyr Ser Gly
            260   265   270

Gly Asn Asp Ser Asn Val Ile Lys Thr Glu Ala Asp Ile Tyr Glu Asp
            275   280   285

His Lys Lys His Ala Ala Ala Ala Ala Ala Ala Gly Gly Gly Ser
    290   295   300

Ile Ile Tyr Thr Thr Ser Asp Pro Asn Gly Val Asn Val Lys Gln Leu

- 69 -

```
305                    310                    315                    320


Pro His Leu Thr Val Pro Gln Lys Leu Asp Pro Asp Leu Tyr Gln Ala
              325             330             335


Asp Lys His Ile Asp Leu Ile Tyr Asn Asp Gly Ser Lys Thr Val Ile
              340             345             350


Tyr Ser Thr Thr Asp Gln Lys Ser Leu Glu Ile Tyr Ser Gly Gly Asp
              355             360             365


Ile Gly Ser Leu Val Ser Asp Gly Gln Val Val Val Gln Ala Gly Leu
         370             375             380


Pro Tyr Ala Thr Thr Thr Gly Ala Gly Gly Gln Pro Val Tyr Ile Val
385             390             395             400


Ala Asp Gly Ala Leu Pro Ala Gly Val Glu Glu His Leu Gln Ser Gly
              405             410             415


Lys Leu Asn Gly Gln Thr Thr Pro Ile Asp Val Ser Gly Leu Ser Gln
              420             425             430


Asn Glu Ile Gln Gly Phe Leu Leu Gly Ser His Pro Ser Ser Ser Ala
              435             440             445


Thr Val Ser Thr Thr Gly Val Val Ser Thr Thr Thr Ile Ser His His
         450             455             460


Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln
465                 470                 475                 480


Gln His Gln Gln Gln Gln Gln His Pro Gly Asp Ile Val Ser Ala Ala
              485             490             495


Gly Val Gly Ser Thr Gly Ser Ile Val Ser Ser Ala Ala Gln Gln Gln
         500             505             510


Gln Gln Gln Gln Leu Ile Ser Ile Lys Arg Glu Pro Glu Asp Leu Arg
         515             520             525


Lys Asp Pro Lys Asn Gly Asn Ile Ala Gly Ala Ala Thr Ala Asn Gly
530             535             540
```

Pro Gly Ser Val Ile Thr Gln Lys Ile Leu His Val Asp Ala Pro Thr
545   550   555   560

Ala Ser Glu Ala Asp Arg Pro Ser Thr Pro Ser Ser Ser Ile Asn Ser
            565   570   575

Thr Glu Asn Thr Glu Ser Asp Ser Gln Ser Val Ser Gly Ser Glu Ser
        580   585   590

Gly Ser Pro Gly Ala Arg Thr Thr Ala Thr Leu Glu Met Tyr Ala Thr
        595   600   605

Thr Gly Gly Thr Gln Ile Tyr Leu Gln Thr Ser His Pro Ser Thr Ala
    610   615   620

Ser Gly Ala Gly Gly Gly Ala Gly Pro Ala Gly Ala Ala Gly Gly Gly
625   630   635   640

Gly Val Ser Met Gln Ala Gln Ser Pro Ser Pro Gly Pro Tyr Ile Thr
            645   650   655

Ala Asn Asp Tyr Gly Met Tyr Thr Ala Ser Arg Leu Pro Pro Gly Pro
            660   665   670

Pro Pro Thr Ser Thr Thr Thr Phe Ile Ala Glu Pro Ser Tyr Tyr Arg
        675   680   685

Glu Tyr Phe Ala Pro Asp Gly Gln Gly Gly Tyr Val Pro Ala Ser Thr
    690   695   700

Arg Ser Leu Tyr Gly Asp Val Asp Val Ser Val Ser Gln Pro Gly Gly
705   710   715   720

Val Val Thr Tyr Glu Gly Arg Phe Ala Gly Ser Val Pro Pro Pro Ala
            725   730   735

Thr Thr Thr Val Leu Thr Ser Val His His Gln Gln Gln Gln Gln
        740   745   750

Gln Gln Gln Gln His Gln Gln Gln Gln Gln Gln Gln His His Gln
    755   760   765

Gln Gln Gln His His Ser Gln Asp Gly Lys Ser Asn Gly Gly Ala Thr
    770   775   780

Pro Leu Tyr Ala Lys Ala Ile Thr Ala Ala Gly Leu Thr Val Asp Leu
785   790   795   800

Pro Ser Pro Asp Ser Gly Ile Gly Thr Asp Ala Ile Thr Pro Arg Asp
         805   810   815

Gln Thr Asn Ile Gln Gln Ser Phe Asp Tyr Thr Glu Leu Cys Gln Pro
        820   825   830

Gly Thr Leu Ile Asp Ala Asn Gly Ser Ile Pro Val Ser Val Asn Ser
      835   840   845

Ile Gln Gln Arg Thr Ala Val His Gly Ser Gln Asn Ser Pro Thr Thr
    850   855   860

Ser Leu Val Asp Thr Ser Thr Asn Gly Ser Thr Arg Ser Arg Pro Trp
865   870   875   880

His Asp Phe Gly Arg Gln Asn Asp Ala Asp Lys Ile Gln Ile Pro Lys
        885   890   895

Ile Phe Thr Asn Val Gly Phe Arg Tyr His Leu Glu Ser Pro Ile Ser
      900   905   910

Ser Ser Gln Arg Arg Glu Asp Asp Arg Ile Thr Tyr Ile Asn Lys Gly
      915   920   925

Gln Phe Tyr Gly Ile Thr Leu Glu Tyr Val His Asp Ala Glu Lys Pro
    930   935   940

Ile Lys Asn Thr Thr Val Lys Ser Val Ile Met Leu Met Phe Arg Glu
945   950   955   960

Glu Lys Ser Pro Glu Asp Glu Ile Lys Ala Trp Gln Phe Trp His Ser
        965   970   975

Arg Gln His Ser Val Lys Gln Arg Ile Leu Asp Ala Asp Thr Lys Asn
      980   985   990

- 72 -

```
Ser Val Gly Leu Val Gly Cys Ile  Glu Glu Val Ser His  Asn Ala Ile
        995                1000                 1005


Ala Val Tyr Trp Asn Pro Leu  Glu Ser Ser Ala Lys  Ile Asn Ile
        1010            1015                 1020


Ala Val Gln Cys Leu Ser Thr  Asp Phe Ser Ser Gln  Lys Gly Gly
        1025            1030                 1035


Leu Pro Leu His Val Gln Ile  Asp Thr Phe Glu Asp  Pro Arg Asp
        1040            1045                 1050


Thr Ala Val Phe His Arg Gly  Tyr Cys Gln Ile Lys  Val Phe Cys
        1055            1060                 1065


Asp Lys Gly Ala Glu Arg Lys  Thr Arg Asp Glu Glu  Arg Arg Ala
        1070            1075                 1080


Ala Lys Arg Lys Met Thr Ala  Thr Gly Arg Lys Lys  Leu Asp Glu
        1085            1090                 1095


Leu Tyr His Pro Val Thr Asp  Arg Ser Glu Phe Tyr  Gly Met Gln
        1100            1105                 1110


Asp Phe Ala Lys Pro Pro Val  Leu Phe Ser Pro Ala  Glu Asp Met
        1115            1120                 1125


Glu Lys Val Gly Gln Leu Gly  Ile Gly Ala Ala Thr  Gly Met Thr
        1130            1135                 1140


Phe Asn Pro Leu Ser Asn Gly  Asn Ser Asn Ser Asn  Ser His Ser
        1145            1150                 1155


Ser Leu Gln Ser Phe Tyr Gly  His Glu Thr Asp Ser  Pro Asp Leu
        1160            1165                 1170


Lys Gly Ala Ser Pro Phe Leu  Leu His Gly Gln Lys  Val Ala Thr
        1175            1180                 1185


Pro Thr Leu Lys Phe His Asn  His Phe Pro Pro Asp  Met Gln Thr
        1190            1195                 1200


Asp Lys Lys Asp His Ile Leu  Asp Gln Asn Met Leu  Thr Ser Thr
```

- 73 -

```
        1205                    1210                    1215

Pro Leu  Thr Asp Phe Gly Pro  Pro Met Lys Arg Gly  Arg Met Thr
         1220                  1225                  1230

Pro Pro  Thr Ser Glu Arg Val  Met Leu Tyr Val Arg  Gln Glu Asn
         1235                  1240                  1245

Glu Glu  Val Tyr Thr Pro Leu  His Val Val Pro Pro  Thr Thr Ile
         1250                  1255                  1260

Gly Leu  Leu Asn Ala Ile Glu  Asn Lys Tyr Lys Ile  Ser Thr Thr
         1265                  1270                  1275

Ser Ile  Asn Asn Ile Tyr Arg  Thr Asn Lys Lys Gly  Ile Thr Ala
         1280                  1285                  1290

Lys Ile  Asp Asp Asp Met Ile  Ser Phe Tyr Cys Asn  Glu Asp Ile
         1295                  1300                  1305

Phe Leu  Leu Glu Val Gln Gln  Ile Glu Asp Asp Leu  Tyr Asp Val
         1310                  1315                  1320

Thr Leu  Thr Glu Leu Pro Asn  Gln
         1325                  1330
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<213>   Drosophila

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gcagcaacat caaatgttag gccaaaatgc acaaaccgcc agcaacaaag gcagcaccaa     180

gcgaacgaaa caacaacagc tccacatacc acaaagagtg gcacattaga agcggccaaa     240

agcagccagc cgagagcatt gtgtaagcca aaggcccaga gagccaggct aaaagccccc     300

agacgcacaa caacaacaac aacaactaaa acagcacaaa gagtggcgaa aggtgcaccc     360

accagcaaaa cagcaacaac ggagcaacca acaacagcag cagcagcagc agcagccaca     420

tttcagttac agctccagac tcccaggttg cagactccca aagcaaacag actccagtcc     480
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- 74 -

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acaacgacta agacgaagat cgaccatcca gaaccggagg gagctaattg cgaacgaaag    720

aaaccacaaa gtgccttcca tcaatccgtt gataagtgat atttattatg tttatacttg    780

ccagcagccg aggcagcaac agcaatagca acaaccatag gggatcacgg catcgatgat    840

cagtccacga ccaagtccta gtgcaatccg gaatccagtt caaattagtt caataagccg    900

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- 76 -

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- 77 -

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Gln His Thr His Ser Arg Leu Gly Val Gly Val Gly Val Gly Ile Leu
            35                  40                  45


Ser Asp Ala Ser Leu Ser Pro Ile Gln Gln Gly Ser Gly Gly His Ser
    50                  55                  60


Gly Gly Gly Asn Thr Asn Ser Ser Pro Leu Ala Pro Asn Gly Val Pro
65                  70                  75                  80


Leu Leu Thr Thr Met His Arg Ser Pro Asp Ser Pro Gln Pro Glu Leu
                85                  90                  95


Ala Thr Met Thr Asn Val Asn Val Leu Asp Leu His Thr Asp Asn Ser
            100                 105                 110


Lys Leu Tyr Asp Lys Glu Ala Val Phe Ile Tyr Glu Thr Pro Lys Val
        115                 120                 125


Val Met Pro Ala Asp Gly Gly Gly Gly Asn Asn Ser Asp Glu Gly His
    130                 135                 140


Ala Ile Asp Ala Arg Ile Ala Ala Gln Met Gly Asn Gln Ala Gln Gln
145                 150                 155                 160


Gln Gln Gln Gln Gln Gln Gln Thr Glu His Gln Pro Leu Ala Lys Ile
                165                 170                 175


Glu Phe Asp Glu Asn Gln Ile Ile Arg Val Val Gly Pro Asn Gly Glu
            180                 185                 190


Gln Gln Gln Ile Ile Ser Arg Glu Ile Ile Asn Gly Glu His His Ile
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Leu Ser Arg Asn Glu Ala Gly Glu His Ile Leu Thr Arg Ile Val Ser
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Asp Pro Ser Lys Leu Met Pro Asn Asp Asn Ala Val Ala Thr Ala Met
225   230   235   240

Tyr Asn Gln Ala Gln Lys Met Asn Asn Asp His Gly Gln Ala Val Tyr
            245   250   255

Gln Thr Ser Pro Leu Pro Leu Asp Ala Ser Val Leu His Tyr Ser Gly
            260   265   270

Gly Asn Asp Ser Asn Val Ile Lys Thr Glu Ala Asp Ile Tyr Glu Asp
        275   280   285

His Lys Lys His Ala Ala Ala Ala Ala Ala Ala Gly Gly Gly Ser
    290   295   300

Ile Ile Tyr Thr Thr Ser Asp Pro Asn Gly Val Asn Val Lys Gln Leu
305   310   315   320

Pro His Leu Thr Val Pro Gln Lys Leu Asp Pro Asp Leu Tyr Gln Ala
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Asp Lys His Ile Asp Leu Ile Tyr Asn Asp Gly Ser Lys Thr Val Ile
            340   345   350

Tyr Ser Thr Thr Asp Gln Lys Ser Leu Glu Ile Tyr Ser Gly Gly Asp
            355   360   365

Ile Gly Ser Leu Val Ser Asp Gly Gln Val Val Val Gln Ala Gly Leu
    370   375   380

Pro Tyr Ala Thr Thr Thr Gly Ala Gly Gly Gln Pro Val Tyr Ile Val
385   390   395   400

Ala Asp Gly Ala Leu Pro Ala Gly Val Glu Glu His Leu Gln Ser Gly
            405   410   415

Lys Leu Asn Gly Gln Thr Thr Pro Ile Asp Val Ser Gly Leu Ser Gln
            420   425   430

Asn Glu Ile Gln Gly Phe Leu Leu Gly Ser His Pro Ser Ser Ser Ala
        435   440   445

Thr Val Ser Thr Thr Gly Val Val Ser Thr Thr Thr Ile Ser His His
        450   455   460

Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln
465   470   475   480

Gln His Gln Gln Gln Gln Gln His Pro Gly Asp Ile Val Ser Ala Ala
                    485   490   495

Gly Val Gly Ser Thr Gly Ser Ile Val Ser Ser Ala Ala Gln Gln Gln
                500   505   510

Gln Gln Gln Gln Leu Ile Ser Ile Lys Arg Glu Pro Glu Asp Leu Arg
                515   520   525

Lys Asp Pro Lys Asn Gly Asn Ile Ala Gly Ala Ala Thr Ala Asn Gly
        530   535   540

Pro Gly Ser Val Ile Thr Gln Lys Ile Leu His Val Asp Ala Pro Thr
545   550   555   560

Ala Ser Glu Ala Asp Arg Pro Ser Thr Pro Ser Ser Ser Ile Asn Ser
                565   570   575

Thr Glu Asn Thr Glu Ser Asp Ser Gln Ser Val Ser Gly Ser Glu Ser
                580   585   590

Gly Ser Pro Gly Ala Arg Thr Thr Ala Thr Leu Glu Met Tyr Ala Thr
                595   600   605

Thr Gly Gly Thr Gln Ile Tyr Leu Gln Thr Ser His Pro Ser Thr Ala
        610   615   620

Ser Gly Ala Gly Gly Gly Ala Gly Pro Ala Gly Ala Ala Gly Gly Gly
625   630   635   640

Gly Val Ser Met Gln Ala Gln Ser Pro Ser Pro Gly Pro Tyr Ile Thr
                645   650   655

- 80 -

Ala Asn Asp Tyr Gly Met Tyr Thr Ala Ser Arg Leu Pro Pro Gly Pro
          660   665   670

Pro Pro Thr Ser Thr Thr Thr Phe Ile Ala Glu Pro Ser Tyr Tyr Arg
          675   680   685

Glu Tyr Phe Ala Pro Asp Gly Gln Gly Gly Tyr Val Pro Ala Ser Thr
    690 .   695   700

Arg Ser Leu Tyr Gly Asp Val Asp Val Ser Val Ser Gln Pro Gly Gly
705   710   715   720

Val Val Thr Tyr Glu Gly Arg Phe Ala Gly Ser Val Pro Pro Pro Ala
              725   730   735

Thr Thr Thr Val Leu Thr Ser Val His His Gln Gln Gln Gln Gln Gln
          740   745   750

Gln Gln Gln Gln His Gln Gln Gln Gln Gln Gln Gln Gln His His Gln
          755   760   765

Gln Gln Gln His His Ser Gln Asp Gly Lys Ser Asn Gly Gly Ala Thr
          770   775   780

Pro Leu Tyr Ala Lys Ala Ile Thr Ala Ala Gly Leu Thr Val Asp Leu
785   790   795   800

Pro Ser Pro Asp Ser Gly Ile Gly Thr Asp Ala Ile Thr Pro Arg Asp
              805   810   815

Gln Thr Asn Ile Gln Gln Ser Phe Asp Tyr Thr Glu Leu Cys Gln Pro
          820   825   830

Gly Thr Leu Ile Asp Ala Asn Gly Ser Ile Pro Val Ser Val Asn Ser
          835   840   845

Ile Gln Gln Arg Thr Ala Val His Gly Ser Gln Asn Ser Pro Thr Thr
    850   855   860

Ser Leu Val Asp Thr Ser Thr Asn Gly Ser Thr Arg Ser Arg Pro Trp
865   870   875   880

His Asp Phe Gly Arg Gln Asn Asp Ala Asp Lys Ile Gln Ile Pro Lys

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                          885                      890                         895

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  Ser Ser Gln Arg Arg Glu Asp Asp Arg Ile Thr Tyr Ile Asn Lys Gly
              915                   920                   925

  Gln Phe Tyr Gly Ile Thr Leu Glu Tyr Val His Asp Ala Glu Lys Pro
          930                   935                   940

  Ile Lys Asn Thr Thr Val Lys Ser Val Ile Met Leu Met Phe Arg Glu
  945                   950                   955                   960

  Glu Lys Ser Pro Glu Asp Glu Ile Lys Ala Trp Gln Phe Trp His Ser
                  965                   970                   975

  Arg Gln His Ser Val Lys Gln Arg Ile Leu Asp Ala Asp Thr Lys Asn
              980                   985                   990

  Ser Val Gly Leu Val Gly Cys Ile Glu Glu Val Ser His Asn Ala Ile
          995                   1000                  1005

  Ala Val Tyr Trp Asn Pro Leu Glu Ser Ser Ala Lys Ile Asn Ile
      1010                  1015                  1020

  Ala Val Gln Cys Leu Ser Thr Asp Phe Ser Ser Gln Lys Gly Gly
      1025                  1030                  1035

  Leu Pro Leu His Val Gln Ile Asp Thr Phe Glu Asp Pro Arg Asp
      1040                  1045                  1050

  Thr Ala Val Phe His Arg Gly Tyr Cys Gln Ile Lys Val Phe Cys
      1055                  1060                  1065

  Asp Lys Gly Ala Glu Arg Lys Thr Arg Asp Glu Glu Arg Arg Ala
      1070                  1075                  1080

  Ala Lys Arg Lys Met Thr Ala Thr Gly Arg Lys Lys Leu Asp Glu
      1085                  1090                  1095

  Leu Tyr His Pro Val Thr Asp Arg Ser Glu Phe Tyr Gly Met Gln
      1100                  1105                  1110
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Asp Phe Ala Lys Pro Pro Val Leu Phe Ser Pro Ala Glu Asp Met
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Glu Lys Val Gly Gln Leu Gly Ile Gly Ala Ala Thr Gly Met Thr
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Phe Asn Pro Leu Ser Asn Gly Asn Ser Asn Ser Asn Ser His Ser
    1145   1150   1155

Ser Leu Gln Ser Phe Tyr Gly His Glu Thr Asp Ser Pro Asp Leu
    1160   1165   1170

Lys Gly Ala Ser Pro Phe Leu Leu His Gly Gln Lys Val Ala Thr
    1175   1180   1185

Pro Thr Leu Lys Phe His Asn His Phe Pro Pro Asp Met Gln Thr
    1190   1195   1200

Asp Lys Lys Asp His Ile Leu Asp Gln Asn Met Leu Thr Ser Thr
    1205   1210   1215

Pro Leu Thr Asp Phe Gly Pro Pro Met Lys Arg Gly Arg Met Thr
    1220   1225   1230

Pro Pro Thr Ser Glu Arg Val Met Leu Tyr Val Arg Gln Glu Asn
    1235   1240   1245

Glu Glu Val Tyr Thr Pro Leu His Val Val Pro Pro Thr Thr Ile
    1250   1255   1260

Gly Leu Leu Asn Ala Ile Glu Asn Lys Tyr Lys Ile Ser Thr Thr
    1265   1270   1275

Ser Ile Asn Asn Ile Tyr Arg Thr Asn Lys Lys Gly Ile Thr Ala
    1280   1285   1290

Lys Ile Asp Asp Asp Met Ile Ser Phe Tyr Cys Asn Glu Asp Ile
    1295   1300   1305

Phe Leu Leu Glu Val Gln Gln Ile Glu Asp Asp Leu Tyr Asp Val
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